



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 107436**

**To: Michael Borin**  
**Location: cm1/12a01/12d01**  
**Art Unit: 1631**  
**Thursday, November 06, 2003**

**Cas Serial Number: 09/960481**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**CM1-1E05**  
**Phone: 308-4994**

**beverly.shears@uspto.gov**

### **Search Notes**

Michael,

Searched Seq. ID 5278 using the oligomer parameters. If you were interested in a size limited search, pls. contact me.

Beverly

09/960481  
Seq. ID 5278

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

M nucleic - nucleic search, using sw model

un on: November 6, 2003, 01:51:23 ; Search time 1392 Seconds  
(without alignments)  
7376.664 Million cell updates/sec

Title: US-09-960-481-5278

Perfect score: 251

Sequence: 1 ggtggcagttgtgtgacaca.....gtaagaaganatcaaccgag 251

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_ete.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	52.6	21.0	1117	8	MTN3	Y08726 M.truncatul
2	52.4	20.9	553	8	AF151726	AF151726 Dianthus
3	51.8	20.6	1182	8	AF313914	AF313914 Petunia x
4	51.8	20.6	1205	6	AX006355	AX006355 Sequence
5	46	18.3	1252	8	AY087516	AY087516 Arabidops
6	45.6	18.2	902	8	AY086047	AY086047 Arabidops
7	45	17.9	879	6	AX06568	AX06568 Sequence
8	45	17.9	910	8	AY113934	AY113934 Arabidops
9	45	17.9	1269	8	AY087836	AY087836 Arabidops
10	45	17.9	1291	8	AY045949	AY045949 Arabidops
11	44.4	17.7	870	8	AY078041	AY078041 Arabidops
12	44.4	17.7	901	8	AY096594	AY096594 Arabidops
13	44.4	17.7	1157	8	AF361825	AF361825 Arabidops
14	44.4	17.7	1172	8	AF419559	AF419559 Arabidops
15	44.4	17.7	1176	8	BT000808	BT000808 Arabidops
16	44.4	17.7	1196	8	AY070412	AY070412 Arabidops
17	40.4	16.1	1124	8	AY116672	AY116672 Arabidops
18	39.8	15.9	1221	8	AY084672	AY084672 Arabidops
19	39.6	15.8	889	8	AY059108	AY059108 Arabidops
20	39.6	15.8	1209	8	AF095641	AF095641 Arabidops
21	39.6	15.8	1279	8	AY057575	AY057575 Arabidops
22	38.2	15.2	934	8	AY064674	AY064674 Arabidops
23	38.2	15.2	1250	8	AY054548	AY054548 Arabidops
24	37.8	15.1	152177	10	AL672064	AL672064 Mouse DNA
25	37.6	15.0	841	11	BY019724	BY019724 S212P6038
26	37.4	14.9	167515	5	AL928980	AL928980 Zebrafish
27	37	14.7	139039	2	AP005322	AP005322 Oryza sat
28	37	14.7	144941	2	AP004837	AP004837 Oryza sat
29	36.2	14.4	134167	9	AC064814	AC064814 Homo sapi
30	36.2	14.4	180013	2	AC121079	AC121079 Mus muscu
31	36.2	14.4	197096	10	AC104329	AC104329 Mus muscu
32	36.2	14.4	231992	2	AC126738	AC126738 Rattus no
33	35.8	14.3	6303	9	HSN803904	HSN803904 Homo sapi
34	35.8	14.3	159476	9	AC090149	AC090149 Homo sapi
35	35.8	14.3	159531	9	AC090575	AC090575 Homo sapi
36	35.8	14.3	169876	9	AC037450	AC037450 Homo sapi
37	35.8	14.3	178743	2	AC136178	AC136178 Rattus no
38	35.8	14.3	203843	2	AC021591	AC021591 Homo sapi
39	35.6	14.2	103699	9	AC034305	AC034305 Homo sapi
40	35.6	14.2	123244	10	BX004791	BX004791 Mouse DNA
41	35.6	14.2	123931	9	AC011404	AC011404 Homo sapi
42	35.6	14.2	147876	2	AC144353	AC144353 Homo sapi
43	35.6	14.2	152303	2	AC143335	AC143335 Homo sapi
44	35.6	14.2	160494	9	AC108080	AC108080 Homo sapi
45	35.6	14.2	169770	9	AC027763	AC027763 Homo sapi

ALIGNMENTS

RESULT 1

MTN3

LOCUS

DEFINITION M.truncatula mRNA for MTN3 gene.

ACCESSION Y08726

VERSION Y08726.1 GI:1619601

KEYWORDS MtN3 gene.

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

REFERENCE 1 (bases 1 to 1117)

AUTHORS

Gamas,P., Niebel Fde,C., Lescure,N. and Cullimore,J.

linear PLN 01-NOV-1997



```
CDS
56. .853
/notes="nectary-specific"
/codon_start=1
/product="NEC1"
/db_xref="GI:11345413"
/translations="MAQLRADDLSFI GLLGNIVSFMVFLAPVPTFYKIKRSSEGY
OALPYMVAFSAGLLYYALRNKAVLIVSINGFGCAIELTYISLFLYAPRKSIFT
GWLMLLELGA LMVPEITYLLAGSHRVMIVGICAINVAVPAAPLSIMRQVIKTS
VEMPFLLSLFTLCATMFFYGFKKDFYAFNPILGFLGIVQMLLYFVYKDSKRI
DDEKSPVREATKSKEGVEIINIEDNSNALQSMKDFSLRSTSK"
ASE COUNT 372 a 209 c 220 g 381 t
ORIGIN
Query Match 20.6%; Score 51.8; DB 8; Length 1182;
Best Local Similarity 70.8%; Pred. No. 0.00055;
Matches 68; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
y 155 TTTCGCTTTGGGATTCAGTAACATTGCTGCTCGTGTGCTTTCTTGGCACCACCTACC 214
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
b 85 TTTCATATTGGCTTCTTGTAATATTGATCATTCATGCTTCTCTAGCACCGGTGCC 144
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
y 215 AACATTTTATAGATTGTTGAAGAGANATCAACCGA 250
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
b 145 AACATTTTACAAAATATATAAAGGAATCATCAGA 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
X006355 Petunia x hybrida
LOCUS Petunia x hybrida
DEFINITION Sequence 4 from Patent WO0004176.
ACCESSION AX006355
VERSION AX006355.1 GI:9994501
KEYWORDS
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
1
Angenent,G.C., Creemers,J. and Kater,M.M.
Process to collect metabolites from modified nectar by insects
Patent: WO 0004176-A 4 27-JAN-2000;
ANGENENT GERIT CORNELIS (NL); CREEMERS JANTINA (NL); KATER MARTIN
MARIA (NL); STICHTING CT VOOR PLANTENVERED (NL)
FEATURES
source
Location/Qualifiers
1. .1205
/organism="Petunia x hybrida"
/mol_type="genomic DNA"
/strain="W115"
/db_xref="taxon:4102"
/tissue_type="nectar gland"
79. .876
/notes="NEC1"
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/protein_id="CAC07355.1"
/db_xref="GI:9994502"
/translations="MAQLRADDLSFI GLLGNIVSFMVFLAPVPTFYKIKRSSEGY
OALPYMVAFSAGLLYYALRNKAVLIVSINGFGCAIELTYISLFLYAPRKSIFT
GWLMLLELGA LMVPEITYLLAGSHRVMIVGICAINVAVPAAPLSIMRQVIKTS
VEMPFLLSLFTLCATMFFYGFKKDFYAFNPILGFLGIVQMLLYFVYKDSKRI
DDEKSPVREATKSKEGVEIINIEDNSNALQSMKDFSLRSTSK"
ASE COUNT 374 a 219 c 229 g 383 t
ORIGIN
Query Match 20.6%; Score 51.8; DB 6; Length 1205;
Best Local Similarity 70.8%; Pred. No. 0.00055;
Matches 68; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
y 155 TTTCGCTTTGGGATTCAGTAACATTGCTGCTCGTGTGCTTTCTTGGCACCACCTACC 214
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
b 108 TTTCATATTGGCTTCTTGTAATATTGATCATTCATGCTTCTCTAGCACCGGTGCC 167
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

CDS
1252 bp mRNA linear PLN 14-APR-2003
Arabidopsis thaliana clone 36264 mRNA, complete sequence.
AY087516
AY087516.1 GI:21406253
FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1252)
Haas,B.J., Volfovsky,N., Town,C.D., Troughan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
22088475
12093376
2 (bases 1 to 1252)
Brover,V., Troughan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
3 (bases 1 to 1252)
Brover,V., Troughan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of
the clones are estimated to be 5'-truncated, less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the Ws or Llaer ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
Genet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.
FEATURES
source
Location/Qualifiers
1. .1252
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/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="36264"
165. .1049
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/protein_id="AAM65058.1"
/db_xref="GI:21593109"
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SLPYSAFLSAMLWIVYAMQKDTAFLLITINARGCVLETIYIVLVSYANKKTRIST
LKVGLGLNPGFAALVVCZLLTGKSGREKVGICVGSVSPAAPLSIMRQVVRTR
SVEMPFLLSLFTISATVWLFGLAIKDFYALNPVLPVLPVLPVLPVLPVLPVLPVLPV
PVAQTKDKSDVSDHSIDIAKLTVIFGAVLDSAVHQPALHPVETKIQLTVEYKSON
MTDPKQINKDVQKQSQV"
BASE COUNT 335 a 269 c 234 g 413 t 1 others
ORIGIN
Query Match 18.3%; Score 46; DB 8; Length 1252;
```





Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Mitanda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Arabidopsis Open Reading Frame (ORF) Clones

Unpublished

2 (bases 1 to 910)

Yamada, K., Banb, J., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Mitanda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Davis, R.W., Ecker, J.R. and Theologis, A.

Direct Submission

Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA': Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

Query Match	17.9%;	Score 45;	DB 8;	Length 910;
Best Local Similarity	62.7%;	Pred. No. 0.045;		
Matches	69;	Conservative 0;	Mismatches 41;	Indels 0;
			Gaps	0;
Qy	141	CACAGTCATCTAGTTTCGCGCTTTGGGATCTCTAGGTAAACATGCCTCCTTCGTGTCGCTTT	200	
Db	19	CACATTTCTCGCTTTTATCTTCGGCATCTTAGGAACGTGATATCCTTCCTTGTTATTC	78	
Qy	201	CTGGCACCACTACCAACATTTTATAGAGTTTGTGAAGAAGANATCAACCGA	250	
Db	79	CTCGCTCCAGTGCCCACTTTTATAGAAATATACAGAGAAATCGACGGA	128	
RESULT 9				
AY087836				
LOCUS	AY087836	1269 bp	mRNA	linear
DEFINITION	Arabidopsis thaliana clone 38843 mRNA, complete sequence.			PLN 14-APR-2003

ORGANISM

Arabioidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1269)

JOURNAL: Genome Biol. 3 (6), RESEARCH0029 (2002)  
MEDLINE: 22088475  
PUBMED: 12093376  
REFERENCE: 2 (bases 1 to 1269)  
AUTHORS: Bouvier V, Treutlein M, Alexandrov N, Li Y, D'Elia J, P and

**AUTHORS** Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavel, R. and Feldmann, K.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,

are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be

**FEATURES**

5' sequences, selection of clones, and sequence assembly.

Location/Qualifiers

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CDS
136..1014
/codon_start=1
/product="serenence-associated protein (SAG2)"
/protein_id="AA065389.1"
/clone="38843"
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Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

## TITLE Arabidopsis cDNA clones

## JOURNAL Unpublished

## REFERENCE

## AUTHORS

2 (bases 1 to 870)  
Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

## Direct Submission

## TITLE

## JOURNAL

Submitted (04-FEB-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

## COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Chan, M.M., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Davis, R.W., Theologis, A., and Ecker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

## FEATURES

## source

1..870

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/chromosome="3"

/clones="U12160"

/note="This clone is in pUNI 51"

ecotype: Columbia"

1..870

/note="MTN3-like protein"

/codon\_start=1

/product="AT3g48740/T8P19\_250"

/protein\_id="AAL77742.1"

/db\_xref="GI:18700264"

/translation="MSLFTNTWAFVFLGLGNISFAVLSVPPTFYRIWKKTTEG  
FQSIYVVAFTSLWLYATQKQKQVLTINAFGCFIETIYSMEFLAYAPAPKML  
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RSVEYMFPSLSLTITISAVILYGLAKDIYVAFPNVLFGALGQMLYVYKCYK  
TSPHLGEKEVEAAKLPEVSLDMLKLTGVSSPVVRQANKCTCGNDRRAIEDGT  
PKHGKQSSAAAT"

210 a 209 c 193 g 258 t

## BASE COUNT

## ORIGIN

Query Match 17.7%; Score 44.4; DB 8; Length 870;  
Best Local Similarity 66.3%; Pred. No. 0.067;  
Matches 63; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

156 TTGGCTTTGGATTCTAGTAACTTCCTCGTGTGCTTTCTGGCAACCACTACCA 215

157 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

34 TTTCGCTTGGCTTCGCGCAACCTATCTCTTTCGCGGTTCCTATCTCTCGTCCCA 93

35 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

216 ACATTTATAGATTGTGAAGAGNATCAACCA 250

217 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

94 ACGTTCTATAGATTGTGAAGAGNATCAACCA 128

## RESULT 12

## AY096594

## LOCUS

## DEFINITION

## SOURCE

## ORGANISM

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

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## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

AY096594 901 bp mRNA linear PLN 18-SEP-2002  
Arabidopsis thaliana putative MTN3 protein (At3g48740) mRNA,  
complete cds.

AY096594

AY096594.1 GI:20465522

FLI CDNA

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Arabidopsis thaliana

Arabidopsis thaliana

Arabidopsis thaliana

Arabidopsis thaliana

Arabidopsis thaliana

Arabidopsis thaliana

Arabidopsis thaliana

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Arabidopsis thaliana

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RSVEYMPFSLTLLTISAVILWLLYGLAKDIYVAFPNVZGFALGALQMLLYVYVYCK
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871..901
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ORIGIN

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Best Local Similarity 66.3%; Pred. No. 0.067;
Matches 63; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 156 TTGCGCTTTGGGATCTAGTACATTCGCTCTTCTGCTGCTTTCTGCACACACTACCA 215
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 TTGTCTTTGGCTTGTCTGCGCAACCTTATCTCTTTCGCGTGTCTCTATCTCTCTGCGCA 93
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QY 216 ACATTTTATAGACTTTGTAAGAAGANATCAACCGA 250
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
94 ACCTTCTATAGGATTGGAAGAGACACACAGAGA 128
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RESULT 13
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LOCUS Arabidopsis thaliana AT3g48740/T8P19_250 mRNA, complete cds.
DEFINITION Arabidopsis thaliana (thale cress)
ACCESSION AF361825.1 GI:13605687
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1157)
Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Banh,J., Bowser,L.,
Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M.,
Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T., Satou,M., Seki,M.,
Southwick,A., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
Unpublished
Direct Submission
2 (bases 1 to 1157)
Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Banh,J., Bowser,L.,
Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M.,
Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T., Satou,M., Seki,M.,
Southwick,A., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
Unpublished
Submitted (19-MAR-2001) Salk Institute Genomic Analysis Laboratory
(SIGAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Shinn,P., Chen,H.,
Cheuk,R., Kim,C.J., Koesema,E., Meyers,M.C., Tracy,S.E., Banh,J.,
Bowser,L., Chung,M.K., Goldsmith,A.D., Jones,T., Karlin-Neumann,G.,
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Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Southwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Davis,R.W., Theologis,A.,
and Ecker,J.R.

Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
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Best Local Similarity 66.3%; Pred. No. 0.065;
Matches 63; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 156 TTGCGCTTTGGGATCTAGTACATTCGCTCTTCTGCTGCTTTCTGCACACACTACCA 215
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122 TTGTCTTTGGCTTGTCTGCGCAACCTTATCTCTTTCGCGTGTCTCTATCTCTCTGCGCA 181
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QY 216 ACATTTTATAGACTTTGTAAGAAGANATCAACCGA 250
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
182 ACCTTCTATAGGATTGGAAGAGACACACAGAGA 216
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RESULT 14
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LOCUS Arabidopsis thaliana AT3g48740/T8P19_250 mRNA, complete cds.
DEFINITION Arabidopsis thaliana (thale cress)
ACCESSION AF419559
VERSION AF419559.1 GI:16930410
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1172)
Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
Unpublished
2 (bases 1 to 1172)
Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
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RIGIN

Query Match 17.7%; Score 44.4; DB 8; Length 1176;  
Best Local Similarity 66.3%; Pred. No. 0.065;  
Matches 63; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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b 124 TTTGTCTTTGGCTTGGCTTCGGCAACCTTATCTCCTTTGGCGTGTCTATCTCTCTGTGCCA 183

y 216 ACATTTTATAGAGTTTGTAAAGAAAGANATCAACCGA 250  
b 184 ACCTTCTATAGGATTTGGAAGAAAGAGACACACAGA 218

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ob time : 1396 secs

GenCore version 5.1.6  
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DM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 23:11:53 : Search time 179 Seconds  
(without alignments)  
3785.246 Million cell updates/sec

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Perfect score: 251  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

searched: 2552756 seqs, 1349719017 residues  
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	54.6	21.8	393	25	ABX22058 Human GDP-mannose
2	54.6	21.8	394	25	ABX22065 Human GDP-mannose
3	51.8	20.6	847	21	AAZ50207 Clone R8 for clon
4	51.8	20.6	847	21	AAZ35498 Petunia nectary-sp
5	51.8	20.6	1205	21	AAZ50200 Petunia hybrida ne
6	51.8	20.6	1205	21	AAZ35493 Petunia nectary-sp
7	46.8	18.6	536	25	ABX18522 Human GDP-mannose
8	46	18.3	1252	21	ABX47147 Arabidopsis thalia

9	45.6	18.2	900	21	ABX47558 Arabidopsis thalia
10	45.6	18.2	902	21	ABX40321 Arabidopsis thalia
11	45.2	18.0	390	25	ABX17994 Human GDP-mannose
12	45	17.9	378	25	ABX18944 Human GDP-mannose
13	45	17.9	389	25	ABX18198 Human GDP-mannose
14	45	17.9	429	21	ABX44368 Arabidopsis thalia
15	45	17.9	879	24	ABZ13458 Arabidopsis thalia
16	45	17.9	1263	21	ABX3408 Arabidopsis thalia
17	44.4	17.7	1177	21	ABX1633 Arabidopsis thalia
18	44.4	17.7	1189	21	ABX41129 Arabidopsis thalia
19	42.8	17.1	985	21	ABX46920 Arabidopsis thalia
20	42	16.7	1159	21	ABX33952 Arabidopsis thalia
21	42	16.7	1159	21	ABX47391 Arabidopsis thalia
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23	39.8	15.9	1221	21	ABX39463 Arabidopsis thalia
24	38.2	15.2	1219	21	ABX49937 Arabidopsis thalia
25	34.2	13.6	1010	21	ABX48836 Arabidopsis thalia
26	34.2	13.6	1011	21	ABX35497 Arabidopsis thalia
27	34.2	13.6	4188	22	ABX98721 Human late stage o
28	34.2	13.6	4188	25	ABT31937 Human breast cance
C 29	33.6	13.4	8328	24	ABX61995 Colon adenocarcino
C 30	33.4	13.3	5928	22	ABX46766 Tumour suppressor
C 31	33.4	13.3	5928	24	ABX34239 Human immune syste
C 32	32.8	13.1	2520	23	ABX68697 DNA encoding novel
C 33	32.8	13.1	2904	23	ABX72979 DNA encoding novel
C 34	32.8	13.1	2916	24	ABQ91973 Human NF-kB activa
C 35	32.8	13.1	3328	24	ABX94856 Human DNA sequence
C 36	32.4	12.9	2701	19	ABX31998 Flax SAD1 gene. L
C 37	32	12.7	3001	21	AAH51715 Chromosome 13q31-q
C 38	31.8	12.7	1893	20	AAV80069 L. helveticus pept
C 39	31.8	12.7	2000	24	ABZ17252 Arabidopsis thalia
C 40	31.6	12.6	484	22	ABX09351 Amplicon DNA compr
C 41	31.4	12.5	297	25	ABX88557 Corn ear-derived p
C 42	31.4	12.5	1035	20	ABX06224 Human secreted pro
C 43	31.4	12.5	1313	24	ABQ54745 Human ovarian anti
C 44	31.4	12.5	3725	23	ABX04282 Drosophila melanog
C 45	31.4	12.5	1503841	24	ABT00010 Human neuregulin 1

# ALIGNMENTS

RESULT 1  
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ID ABX22058 standard; cDNA; 393 BP.  
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AC ABX22058;  
XX  
DT 10-FEB-2003 (first entry)  
XX  
DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #4115.  
XX  
KW Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;  
KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;  
KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;  
KW complex carbohydrate; gene replacement therapy; immunosuppressive;  
KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;  
KW antiasthmatic; vasotropic.  
XX  
OS Homo sapiens.  
XX  
PN US2002110548-A1.  
XX  
PD 15-AUG-2002.  
XX  
PF 11-JUN-2001; 2001US-0878574.  
XX  
PR 22-NOV-1996; 96US-0753233.  
XX  
PR 03-DEC-1997; 97US-0984246.  
XX  
PR 09-SEP-1998; 98US-0149674.  
XX  
PR 14-JUN-1999; 99US-0333177.  
XX  
PA (GEMY ) GENETICS INST INC.







DR WPI; 2000-108438/16.  
 DR P-PSDB; AAY44803.  
 XX  
 XX New DNA encoding Petunia hybrida nectary-specific proteins, useful for,  
 XX e.g. producing modified honey -  
 XX  
 XX Claim 8; Page 42; 93pp; English.  
 XX  
 XX The present sequence is a cDNA encoding nectary-specific protein NEC1.  
 XX It was isolated from nectaries of Petunia hybrida strain W115 using mRNA  
 XX Differential Display system. NEC1 resembles membrane protein and is  
 XX strongly expressed in the nectaries of P. hybrida.  
 XX A DNA sequence from the promoter region upstream of  
 XX nectary-specific expressed sequence e.g. NEC1 and FBPI5 DNAs is used in  
 XX a recombinant DNA construct comprising a DNA encoding a metabolite  
 XX preferably recombinant protein, a DNA encoding a signal peptide that  
 XX targets the recombinant protein to the nectar and optionally a signal  
 XX sequence functional in plants for the transcription termination and  
 XX polyadenylation of an RNA molecule. The DNA construct is useful for  
 XX producing transgenic plants which excrete recombinant proteins in its  
 XX nectar. The nectar is processed into honey by insects (preferably bees)  
 XX and the desired protein is easily recovered from it. The recombinant  
 XX proteins are useful for pharmaceutical purposes, as enzymes for biotests  
 XX and antioxidants for food additives.  
 XX  
 XX Sequence 1205 BP; 374 A; 219 C; 229 G; 383 T; 0 other;  
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 XX Query Match 20.6%; Score 51.8; DB 21; Length 1205;  
 XX Best Local Similarity 70.8%; Pred. No. 4.4e-06;  
 XX Matches 68; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
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 XX QY 155 TTTCGCCCTTTGGGATTCTAGGTAACATTGCGCTTCCTGCTGCTTCTCGCACCACTACC 214  
 XX 108 TTTCATATTGGCCCTTCTGGTAATATTGTATCATTCATGCTTCTCCTAGCACCCGCGCC 167  
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 XX QY 215 AACATTTTATAGAGTTTGTAAAGAGANATCAACCGA 250  
 XX 168 AACATTTTACAAATATATAAAGGAATCATCAGA 203  
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 XX RESULT 6  
 XX ID AAZ35493 standard; cDNA; 1205 BP.  
 XX AC AAZ35493;  
 XX DT 11-APR-2000 (first entry)  
 XX QX Petunia nectary-specific NEC1 cDNA.  
 XX DE NEC1; nectary; nectar; transgenic plant; honey; ds.  
 XX CS Petunia hybrida.  
 XX  
 XX Key Location/Qualifiers  
 XX FH 79..876  
 XX FT CDS /\*tag= a  
 XX FT  
 XX  
 XX PN EP974667-A1.  
 XX  
 XX XX 26-JAN-2000.  
 XX PD  
 XX PF 16-JUL-1998; 98EP-0202375.  
 XX PR 16-JUL-1998; 98EP-0202375.  
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 XX (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.  
 XX PA  
 XX Creemers J, Angenent GC, Kater MM;  
 XX  
 XX WPI; 2000-108400/10.  
 XX DR P-PSDB; AAY58647.  
 XX

PT Novel DNA sequences used to produce modified honey, the metabolites of  
 PT which can be isolated and purified -  
 XX  
 XX Claim 2; Page 16; 56pp; English.  
 XX  
 XX The present sequence is that of Petunia hybrida strain W115 NEC1  
 XX cDNA, as produced from 2 overlapping partial clones (see AAZ35497-98)  
 XX obtained by differential display RT-PCR and RACE PCR. The NEC1  
 XX gene encodes a 265-amino acid protein (see AAY58647). NEC1 is highly  
 XX expressed in the nectaries of petunia and weakly expressed in the  
 XX stamens. The present invention provides a method for producing  
 XX recombinant proteins in honey. The honey is manufactured by insects,  
 XX preferably honeybees, that collect the nectar of transgenic plants.  
 XX The NEC1 gene and its promoter (see AAZ35496) can be utilised in  
 XX expression cassettes for the production of transgenic plants that  
 XX produce a protein of interest in their nectar. The function of  
 XX NEC1 has not yet been determined.  
 XX  
 XX SQ Sequence 1205 BP; 374 A; 219 C; 229 G; 383 T; 0 other;  
 XX  
 XX Query Match 20.6%; Score 51.8; DB 21; Length 1205;  
 XX Best Local Similarity 70.8%; Pred. No. 4.4e-06;  
 XX Matches 68; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
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 XX QY 155 TTTCGCCCTTTGGGATTCTAGGTAACATTGCGCTTCCTGCTGCTTCTCGCACCACTACC 214  
 XX 108 TTTCATATTGGCCCTTCTGGTAATATTGTATCATTCATGCTTCTCCTAGCACCCGCGCC 167  
 XX  
 XX QY 215 AACATTTTATAGAGTTTGTAAAGAGANATCAACCGA 250  
 XX 168 AACATTTTACAAATATATAAAGGAATCATCAGA 203  
 XX  
 XX RESULT 7  
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 XX ID ABX18522 standard; cDNA; 536 BP.  
 XX AC ABX18522;  
 XX DT 10-FEB-2003 (first entry)  
 XX QX Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #579.  
 XX DE  
 XX KW Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;  
 XX cellular fucosylation; glycoconjugate fucosylation; transplant rejection;  
 XX arthritis; asthma; sepsis; reperfusion injury; stroke; infection;  
 XX complex carbohydrate; gene replacement therapy; immunosuppressive;  
 XX antiinflammatory; antiarthritic; antibacterial; cerebroprotective;  
 XX antiasthmatic; vasotropic.  
 XX KW  
 XX OS Homo sapiens.  
 XX  
 XX PN US2002110548-A1.  
 XX  
 XX PD 15-AUG-2002.  
 XX  
 XX PF 11-JUN-2001; 2001US-0878574.  
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 XX PR 22-NOV-1996; 96US-0753233.  
 XX PR 03-DEC-1997; 97US-0984246.  
 XX PR 09-SEP-1998; 98US-0149674.  
 XX PR 14-JUN-1999; 99US-0333177.  
 XX  
 XX (GEMY ) GENETICS INST INC.  
 XX  
 XX Sullivan F, Kriz R, Kumar R;  
 XX  
 XX WPI; 2003-066673/06.  
 XX  
 XX New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)  
 XX peptide, for manufacturing complex carbohydrates, or as targets for  
 XX screening GM4,6D antagonists for treating e.g. arthritis, or transplant  
 XX rejection -  
 XX

X S Disclosure; SEQ ID NO 581; 6pp; English.

X C The invention relates to a composition comprising a human GDP-mannose 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences ABX17942-ABX17944 and ABX17947-ABX3716 represent DNA molecules encoding human GM4,6D peptides of the invention.

X C Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

X Q Sequence 536 BP; 128 A; 123 C; 104 G; 180 T; 1 other;

Query Match 18.6%; Score 46.8; DB 25; Length 536;  
Best Local Similarity 61.0%; Pred. No. 0.00012;  
Matches 75; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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79 CATGACCATGTCACAGTCTTGGCGCTTTGTCTCGCGCTTATGGGCAACATCATCTC 138  
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188 CTTCGTGTCCTTCTGGCACCACCTACCAACATTTATAGAGTTTGTAAAGAGANATCAAC 247  
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139 CTTCGTGAGTCTCTGCTCCATTCGCAACCTTTATCAAACTACCAAGAGAAATCCAC 198  
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248 CGA 250  
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199 TGA 201

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X Hybridisation assay; genetic mapping; gene expression control;  
X protein identification; signal transduction pathway;  
X metabolic pathway; promoter; termination sequence; ss.  
X Arabidopsis thaliana.  
X EP1033405-A2.  
X 06-SEP-2000.  
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Query March 18.3%; Score 46; DB 21; Length 1252;
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XX AC AAC47558;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54267.
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway;
XX KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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QY 215 AACATTTTATAGAGTTGTAAGAGANATCAAC 247
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AC AAC40321;
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27883.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 09-MAR-1999; 99US-0123180.
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PR 29-MAR-1999; 99US-0126264.
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PR 06-APR-1999; 99US-0127462.
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Query Match 18.2%; Score 45.6; DB 21; Length 902;
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Matches 63; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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Db 71 TTTTCTCTTTGGTCTCTTAGGCACCAFTGTGCTTTTGGGGTGTCTTGTGCACCACTGCC 130

QY 215 AACATTTATAGAGTTGTGAAGAGANATCAAC 247
Db 131 AACGTTTATGGGATATACAGAGAAATCATC 163

RESULT 11
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ID ABX17994 standard; cDNA; 390 BP.
AC ABX17994;
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DT 10-FEB-2003 (first entry)
XX
DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #51.
XX
KW Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
KW complex carbohydrate; gene replacement therapy; immunosuppressive;
KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
KW antiasthmatic; vasotropic.
XX
OS Homo sapiens.
XX
PN US2002110548-A1.
XX
PD 15-AUG-2002.
XX
PF 11-JUN-2001; 2001US-0878574.
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PR 22-NOV-1996; 96US-0753233.
PR 03-DEC-1997; 97US-0984246.
PR 09-SEP-1998; 98US-0149674.
PR 14-JUN-1999; 99US-0333177.
XX
PA (GEM ) GENETICS INST INC.
XX
PI Sullivan F, Kriz R, Kumar R;
XX
XX WPI; 2003-066673/06.
XX
PT New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
PT peptide, for manufacturing complex carbohydrates, or as targets for
PT screening GM4,6D antagonists for treating e.g. arthritis, or transplant
PT rejection -
XX
PS Disclosure; SEQ ID NO 53; 6pp; English.
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Qy 201 CTGGCACCCTCCCAACATTTTATAGATTTGTAAGAAGANATCAACCGA 250
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 213 CTGCTCCAGTGCACACTTTTATAGATATATACAGAGAAATCGACCGA 262
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RESULT 15

ID ABZ13458 standard; DNA; 879 BP.

XX AC ABZ13458;

XX XX 21-JAN-2003 (first entry)

XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1263.

XX XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX OS Arabidopsis thaliana.

XX PN W0200216655-A2.

PD 28-FEB-2002.

XX XX 24-AUG-2001; 2001WO-US26685.

XX XX 24-AUG-2000; 2000US-227866P.

PR 26-JAN-2001; 2001US-26467P.

PR 22-JUN-2001; 2001US-300111P.

XX

(SCRI ) SCRIPPS RES INST.  
(SYGN ) SYNGENTA PARTICIPATIONS AG.  
Harper JF, Kreps J, Wang X, Zhu T;  
WPI; 2002-304127/34.  
Identifying a stress condition to which a plant cell has been exposed  
and producing plants with increased tolerance to these abiotic stresses  
Claim 15; SEQ ID NO 1263; 577pp + Sequence Listing; English.  
The invention relates to identifying a stress condition to which a plant  
cell has been exposed, comprising:  
(a) contacting nucleic acid representative of expressed polynucleotides  
in the plant cell with an array or probes representative of the plant  
cell genome; and  
(b) detecting a profile of expressed polynucleotides in the plant cell  
characteristic of a stress response. The method is useful in the  
production of transgenic plants, cells and seeds and in producing plants  
with increased tolerance to abiotic stress. The present sequence is that  
of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used  
in methods of the invention.  
Note: The sequence data for this patent is not represented in the printed  
specification but is based on sequence information supplied to Derwent by  
the European Patent Office.

Sequence 879 BP; 215 A; 199 C; 195 G; 270 T; 0 other;  
Query Match 17.9%; Score 45; DB 24; Length 879;  
Best Local Similarity 62.7%; Pred. No. 0.00051;  
Matches 69; Conservative 0; Mismatches 41; Indels 0; Gaps 0;  
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201 CTGGCACCCTACCAACATTTTATAGATTTTGTAAAGAGNATCAACCGA 250  
79 CTCGCTCCAGTGCCCACTTTTATAGAATATACAAAGAGAAAATCGACGGA 128

Search completed: November 6, 2003, 03:23:19  
Job time : 181 secs

GenCore version 5.1.6  
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M nucleic - nucleic search, using sw model

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itl: US-09-960-481-5278

effect score: 251  
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coring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

searched: 569978 seqs, 220691566 residues

total number of hits satisfying chosen parameters: 1139956

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCURS.COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
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2	32	12.7	3001	4	US-09-539-333D-127
3	31.6	12.6	484	4	US-09-679-409-57
4	31.4	12.5	297	4	US-09-313-294A-7017
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6	31.2	12.4	954	3	US-09-265-315-88
7	31.2	12.4	954	3	US-09-265-315-88
8	31.2	12.4	954	3	US-09-265-315-88
9	31.2	12.4	3211	1	US-07-674-287B-1
10	31.2	12.4	3211	2	US-08-436-900A-1
11	31	12.4	1230025	4	US-09-198-452A-1
12	30.8	12.3	3645	4	US-08-999-689A-3
13	30.2	12.0	662	3	US-09-328-111-623
14	30	12.0	2082	1	US-08-920-812-3
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18	30	12.0	2082	2	US-08-920-828-3
19	30	12.0	56516	2	US-08-996-306-1
20	30	12.0	56516	3	US-09-338-907-1
21	30	12.0	56516	3	US-09-218-207-1
22	30	12.0	56520	3	US-09-338-907-179
23	30	12.0	56520	4	US-09-218-207-179
24	29.8	11.9	546	4	US-09-495-050A-88
25	29.6	11.8	3260	1	US-07-674-287B-3
26	29.6	11.8	3260	2	US-08-436-900A-3
27	29.6	11.8	580073	4	US-08-545-528D-1

28	29.2	11.6	42571	4	US-09-810-347-3	Sequence 3, Appli
c 29	29	11.6	1542	5	PCT-US96-12545-4	Sequence 4, Appli
30	29	11.6	1886	4	US-08-936-165A-224	Sequence 224, App
c 31	29	11.6	5390	5	PCT-US96-12545-5	Sequence 5, Appli
c 32	28.8	11.5	413	4	US-09-615-192A-142	Sequence 142, App
c 33	28.8	11.5	489	2	US-08-975-316-82	Sequence 82, Appl
c 34	28.8	11.5	489	4	US-08-615-192A-82	Sequence 82, Appl
c 35	28.8	11.5	8321	3	US-08-680-506-1	Sequence 1, Appli
c 36	28.8	11.5	48974	3	US-08-920-422-17	Sequence 17, Appl
37	28.4	11.3	38844	4	US-08-734-675-3	Sequence 3, Appli
38	28.2	11.2	3781	3	US-08-688-988-5	Sequence 5, Appli
39	28	11.2	1018	3	US-08-896-095-2	Sequence 2, Appli
c 40	28	11.2	36651	4	US-09-738-894A-3	Sequence 3, Appli
c 41	28	11.2	36651	4	US-09-964-469-3	Sequence 3, Appli
42	28	11.2	112132	4	US-09-741-150-3	Sequence 3, Appli
c 43	28	11.2	162450	4	US-09-345-882-1	Sequence 1, Appli
c 44	27.8	11.1	721	4	US-09-324-803C-1	Sequence 1, Appli
45	27.8	11.1	961	5	PCT-US94-02889-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOVLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 INMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZ9pt-Fls  
US-08-232-463-14

Query Match 13.9%; Score 35; DB 1; Length 7218;





APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
TITLE OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/265,315  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 954 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-265-315-88

Query Match 12.4%; Score 31.2; DB 3; Length 954;  
Best Local Similarity 41.9%; Pred. No. 1.3;  
Matches 96; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 3 TGGCAGTTGTGTGCACACAGAAATTAAGCTAGAGCTTCATAGTTCTTCTTCTCTCAC 62  
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QY 63 CTTCCTCTCTCCCTTCACACAGAAATTAAGCTAGAGCTTCATAGTTCTTCTTCTCAC 122  
DB 167 GCTTCACAGTGTGATGCTGTTTATGATTAATGAATACTAGCTAT 226  
QY 123 NNTTCCAAACCATGTCACAGTCTATCTAGTTTGGCTTTGGGATTTCTAGGTAACT 182  
DB 227 ATTTATAAGGTAGAAAGGGTTTGTGTTAGTGTAGTCAATGATTTATACATAAAG 286  
QY 183 GCCTCTCTGTTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTT 231  
DB 287 GCCCGTTTTTATGTTAGTAAATTAATGTAATACTTGAATAATTTATAGTTTTT 335

## RESULT 7

US-09-265-315-88  
; Sequence 88, Application US/09265315  
; Patent No. 6187541  
; GENERAL INFORMATION:  
; APPLICANT: Benton, Bret

APPLICANT: Lee, Ving J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/265,315  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 954 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-265-315-88

Query Match 12.4%; Score 31.2; DB 3; Length 954;  
Best Local Similarity 41.9%; Pred. No. 1.3;  
Matches 96; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 3 TGGCAGTTGTGTGCACACAGAAATTAAGCTAGAGCTTCATAGTTCTTCTTCTCAC 62  
DB 107 TGAGAGTCTGCTGAACGTAATTAATCTATGTTTAAATGAATACTAGCTAT 166  
QY 63 CTTCCTCTCTCCCTTCACACAGAAATTAAGCTAGAGCTTCATAGTTCTTCTTCTCAC 122  
DB 167 GCTTCACAGTGTGATGCTGTTTATGATTAATGAATACTAGCTAT 226  
QY 123 NNTTCCAAACCATGTCACAGTCTATCTAGTTTGGCTTTGGGATTTCTAGGTAACT 182  
DB 227 ATTTATAAGGTAGAAAGGGTTTGTGTTAGTGTAGTCAATGATTTATACATAAAG 286  
QY 183 GCCTCTCTGTTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTT 231  
DB 287 GCCCGTTTTTATGTTAGTAAATTAATGTAATACTTGAATAATTTATAGTTTTT 335

## RESULT 8

US-09-266-417-88





[illegible]

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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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Query Match 12.4%; Score 31; DB 4; Length 1230025;  
Best Local Similarity 47.1%; Pred. No. 16;  
Matches 49; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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Db 76265 CTTTTTCTTTCTTCTACATATGAGAGCATATAAATAATTATTTCAAAGCACATTGCTGG 76206
QY 123 NNTTCCAAACCATGTCCACAGTCATCTAAGTTTCGGCTTTGG 166
Db 76205 AATCAACGCCACGTATCTAGAGACTAAGTTCTCTCTATAG 76162
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## RESULT 12

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US-08-999-689A-3
Sequence 3, Application US/08999689A
Patent No. 6541615
GENERAL INFORMATION:
APPLICANT: ULLRICH, AXEL
APPLICANT: KHARITONENKOV, ALEXEI
APPLICANT: CHEN, ZHENGJUN
TITLE OF INVENTION: SIRP PROTEINS AND USES THEREOF
FILE REFERENCE: 038602/0548
CURRENT APPLICATION NUMBER: US/08/999,689A
CURRENT FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/030,964
PRIOR FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 3645
TYPE: DNA
ORGANISM: Mus sp.
US-08-999-689A-3
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Query Match 12.3%; Score 30.8; DB 4; Length 3645;  
Best Local Similarity 48.4%; Pred. No. 2.8;  
Matches 44; Conservative 0; Mismatches 47; Indels 0; Gaps 0;



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 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/920,827  
 FILING DATE: 29-AUG-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/362,577  
 FILING DATE: 27-MAR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rita-Laures, Li-Hsien  
 REGISTRATION NUMBER: 33,547  
 REFERENCE/DOCKET NUMBER: 19036/32420  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2082 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 ORIGINAL SOURCE:  
 ORGANISM: Staphylococcus aureus  
 STRAIN: Clinical Isolate SA-36  
 S-08-920-827-3

Query Match 12.0%; Score 30; DB 1; Length 2082;  
 Best Local Similarity 43.7%; Pred.No. 4.1;  
 Matches 66; Conservative 0; Mismatches 85; Indels 0; Gaps 0;  
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 b 58 GGTGTGAAGTGTATATCTGTATTAAATAACCATGTCATTCACTTCTCATTGTGA 117  
 y 61 ACCTTCCTCTCTCCCTTCAGACAAAGGACAAAATCNNNNNNNNNNNNNNNNNNNN 120  
 b 118 ACAAGTCTCCGTCATATAAAATAATGGTACGACATCAATTTTGTACCGTTTCGAG 177  
 y 121 NNNNTCCAAAACCATGTCACAGTCACT 151  
 b 178 ATGCTTTCTAAATCATGTGTAATAACTAATCT 208

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 Job time : 54 sec

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

nucleic - nucleic search, using sw model

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           4171.512 Million cell updates/sec

file:      US-09-960-481-5278
reflect score: 251
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arched:    2141354 seqs, 1595478979 residues

total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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                Maximum Match 100%
                Listing first 45 summaries

Database : Published Applications NA: *

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11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	46.8	18.6	536	10	US-09-878-574-581	Sequence 581, A	
4	45.2	18.0	390	10	US-09-878-574-53	Sequence 53, A	
5	45	17.9	378	10	US-09-878-574-1003	Sequence 1003, A	
6	45	17.9	389	10	US-09-878-574-257	Sequence 257, A	
7	45	17.9	879	10	US-09-938-842A-1263	Sequence 1263, A	
8	41.4	16.5	438	9	US-09-770-444-965	Sequence 965, A	
9	34.2	13.6	4188	14	US-10-176-847-87	Sequence 87, A	
10	33.8	13.5	612	12	US-10-027-632-94170	Sequence 94170, A	
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14	33.6	13.4	89328	12	US-09-873-367C-332	Sequence 332, A	
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c 20	33.4	13.3	969	13	US-10-027-632-9097	Sequence 9097, Ap
c 21	33.4	13.3	5928	12	US-10-311-455-2212	Sequence 2212, Ap
22	33.2	13.2	402850	11	US-09-844-653-5	Sequence 5, Appli
23	33	13.1	735	12	US-10-027-632-174320	Sequence 174320, A
24	33	13.1	735	12	US-10-027-632-174321	Sequence 174321, A
25	33	13.1	735	13	US-10-027-632-174320	Sequence 174320, A
26	33	13.1	735	13	US-10-027-632-174321	Sequence 174321, A
c 27	32.8	13.1	598	12	US-10-027-632-81002	Sequence 81002, A
c 28	32.8	13.1	598	12	US-10-027-632-301748	Sequence 301748, A
c 29	32.8	13.1	598	13	US-10-027-632-81002	Sequence 81002, A
c 30	32.8	13.1	598	13	US-10-027-632-301748	Sequence 301748, A
c 31	32.8	13.1	2916	12	US-10-024-298A-124	Sequence 124, App
c 32	32.8	13.1	2916	12	US-10-042-211A-124	Sequence 134, App
c 33	32.8	13.1	3290	10	US-09-981-353-172	Sequence 172, App
c 34	32.8	13.1	3290	11	US-09-919-03-164	Sequence 164, App
c 35	32.8	13.1	3328	12	US-10-240-965-111	Sequence 111, App
c 36	32.4	12.9	810	12	US-10-027-632-29936	Sequence 29936, A
c 37	32.4	12.9	810	12	US-10-027-632-29937	Sequence 29937, A
c 38	32.4	12.9	810	13	US-10-027-632-29936	Sequence 29936, A
c 39	32.4	12.9	810	13	US-10-027-632-29937	Sequence 29937, A
40	32.2	12.8	663	12	US-10-027-632-214541	Sequence 214541, A
41	32.2	12.8	663	12	US-10-027-632-214542	Sequence 214542, A
42	32.2	12.8	663	12	US-10-027-632-214543	Sequence 214543, A
43	32.2	12.8	663	12	US-10-027-632-214544	Sequence 214544, A
44	32.2	12.8	663	13	US-10-027-632-214541	Sequence 214541, A
45	32.2	12.8	663	13	US-10-027-632-214542	Sequence 214542, A

## ALIGNMENTS

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RESULT 1
US-09-878-574-4117
; Sequence 4117, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 4117
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: L1B3028-001-Q1-B1-C2
US-09-878-574-4117

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Query Match      21.8%; Score 54.6; DB 10; Length 393;
Best Local Similarity 66.1%; Pred. No. 1.9e-07;
Matches 78; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY    133 CCATGTCACAGTCATCTTAAGTTTGCCTTTGGGATTCTAGGTAACATTGCTCCTTCG 192
       |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db     71 CAATTCTCGATCATGAATCGTTTGTGATCTTTGGTCTCGTAGTAACTATGTGTCATTCA 130

QY    193 TGTGGTTTCTGGCACCACTACCACAATTTTATAGACTTTGTAGAAGANATCAACCGA 250
       |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db     131 TGGTGTCTTAGCACCCCTTGCCAACCTTCTATACAAATTTACAAGAAGAATCATCAGA 188

RESULT 2
US-09-878-574-4124
Sequence 4124. Application US/09878574

```

Patent No. US20020110548A1

GENERAL INFORMATION:  
APPLICANT: Byrum, Joseph R.  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Thompson, Michael D.  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(15401)B  
CURRENT APPLICATION NUMBER: US/09/878,574  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 09/333,535  
PRIOR FILING DATE: 1999-06-14  
NUMBER OF SEQ ID NOS: 15775  
SEQ ID NO 4124  
LENGTH: 394  
TYPE: DNA  
ORGANISM: Glycine max  
OTHER INFORMATION: Clone ID: LIB3028-001-Q1-B1-A10  
1-09-878-574-4124

Query Match 21.8%; Score 54.6; DB 10; Length 394;  
Best Local Similarity 66.1%; Pred. No. 1.9e-07;  
Matches 78; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

133 CCATGTCGCACAGTCATCTAAGCTTTGCGCTTTGGGATCTAGGTAAACATGTGCTCTCTCG 192  
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193 TGTGCTTTCTGGCACACTACCAACATTTATAGAGTTTGTAAAGAAGNATCAACCGA 250  
131 TGGTCTTTTAGCACCCCTTGCCAACTTCTATACAAATTTACAAGAAGAAATCATCAGA 188

RESULT 3  
3-09-878-574-581  
Sequence 581, Application US/09878574  
Patent No. US20020110548A1

GENERAL INFORMATION:  
APPLICANT: Byrum, Joseph R.  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Thompson, Michael D.  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(15401)B  
CURRENT APPLICATION NUMBER: US/09/878,574  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 09/333,535  
PRIOR FILING DATE: 1999-06-14  
NUMBER OF SEQ ID NOS: 15775  
SEQ ID NO 581  
LENGTH: 536  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)--(536)  
OTHER INFORMATION: unsure at all n locations  
OTHER INFORMATION: Clone ID: LIB3028-049-Q1-B1-A7  
3-09-878-574-581

Query Match 18.6%; Score 46.8; DB 10; Length 536;  
Best Local Similarity 61.0%; Pred. No. 7.3e-05;  
Matches 75; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

128 CAAACACCATGTCCCAAGTCATCTAAGTTTCGCCCTTTGGATTTCTAGGTAAACATTCCTC 187  
79 CATGACCATGTCATCGGAGTCTTGGGCTTTTGTCTCGCGTTATGGGCAACATCATCTC 138

188 CTTTCGTGCTTTCTGGCACCACTACCAACATTTATAGAGTTTGTAAAGAAGNATCAAC 247  
139 CTTTGAAGTGTCTTGGCTCCATTTGCCAACCTTTTATCAAAATCTACAAGAAGAAATCCAC 198

248 CGA 250

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Db      199 TGA 201
||
RESULT 4
US-09-878-574-53
; Sequence 53, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIORITY APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 53
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-G8
US-09-878-574-53

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Best Local Similarity 60.2%; Pred. No. 0.00021;
Matches   74; Conservative    0; Mismatches  49; Indels    0; Gaps    0;

QY      128 CAAACACCATGTCGCCAGCATCTAAAGTTTGCCTTTGGCGATTCTAGGTAAACATTGCCTC 187
        ||| |||||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB       76 CATGCCATGCATCGGAGTCTTGCGCTTTTGTCTTCGGCGTTATGGCAACATCATCTC 135

QY      188 CTTCGTGCTCTTCTGGCACCACTACCAAATTATTAAGTTTGTAAAGAAGNATCAAC 247
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB       136 CTTTGGAGTGTTCCCTTGCTCCATTGCCAACGTTTTACCAATCTACAAGAAGAAATCCAC 195

QY      248 CGA 250
        ||
DB       196 TGA 198

RESULT 5
US-09-878-574-1003
; Sequence 1003, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIORITY APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1003
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-043-Q1-B1-C9
US-09-878-574-1003

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Best Local Similarity 48.5%; Pred. No. 0.00024;
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QY      84 AAAGGCACAAAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 143
        ||| |||||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

M nucleic - nucleic search, using sw model

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oring table: IDENTITY\_NUC  
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total number of hits satisfying chosen parameters: 45562784

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

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5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	212	84.5	575	12	BM093555	BM093555 sajl0e11.
3	206	82.1	450	13	BU090931	BU090931 su09e10.y
4	200	79.7	473	10	BE804090	BE804090 sr75f12.y

5	200	79.7	531	12	BM887247	BM887247 sam36a12.
6	200	79.7	580	12	BM520189	BM520189 sak90b05.
7	194	77.3	389	10	BF068522	BF068522 st83b03.y
8	193.6	77.1	457	10	BG041196	BG041196 sv31a02.y
9	192.8	76.8	578	12	BM886347	BM886347 sam15d12.
10	191	76.1	218	13	BU764411	BU764411 sae01a10.
11	191	76.1	593	13	BU764490	BU764490 sae02c05.
12	190.2	75.8	458	13	BU090543	BU090543 eu06b06.y
13	189.4	75.5	565	12	BF893295	BF893295 sai64a12.
14	189	75.3	582	12	BM731308	BM731308 sal70c07.
15	170.8	68.0	569	12	BM891461	BM891461 sam27f05.
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17	160.6	64.0	632	10	BF425570	BF425570 su44d05.y
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23	111.4	44.4	645	14	CA847674	CA847674 EST0582 t
24	100	39.8	564	12	BM085196	BM085196 saj33e03.
25	100	39.8	619	10	BF324448	BF324448 su24h10.y
26	76	30.3	252	10	BE806703	BE806703 se84c12.y
27	76	30.3	480	10	BE806709	BE806709 se84d06.y
28	76	30.3	532	10	BG507393	BG507393 sac58e10.
29	76	30.3	628	14	CA801562	CA801562 sau07f01.
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32	66.8	26.6	658	10	EG452436	EG452436 NF080d08L
33	66.2	26.4	451	14	CA800198	CA800198 sat79c06.
34	65.4	26.1	325	10	BE323370	BE323370 NF006f10P
35	65.4	26.1	635	10	BG456823	BG456823 NF097R07P
36	63.4	25.3	695	10	BG454886	BG454886 NF108f10L
37	63.2	25.2	605	10	BE347808	BE347808 sp05h06.y
38	60.2	24.0	679	13	BQ505113	BQ505113 EST612528
39	60.2	24.0	757	10	EG592948	EG592948 EST49a626
40	59.2	23.6	412	10	BF324294	BF324294 su23c09.y
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#### ALIGNMENTS

RESULT 1

BM891617

LOCUS

DEFINITION

sequence.

BM891617

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 554)

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna

A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,

Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers

Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk

R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann

R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine







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/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl057-2770"  
/tissue\_type="Degenerating cotyledons, 2 week old seedling"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl057"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 2 week old seedlings from PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 156 a 124 c 119 g 181 t  
ORIGIN  
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Best Local Similarity 88.3%; Pred. No. 3.2e-40;  
Matches 212; Conservative 0; Mismatches 26; Indels 2; Gaps 1;  
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b 1 GTGACACAGAAATTAAGCTAGAGCTTCATAGTTCTTCTTTCTACCTCCTCTTC 60  
y 73 TCCCTTCAGACAAAGGACAAAATC-NNNNNNNNNNNNNNNNNNNNNNNNNNNN 130  
b 61 TCCCTTCAGACAAAGGACAAAATCAGTGTGAGAGAGAGAGAGAAATTCCAA 120  
y 131 AACCATGTCACAGCTATCTAAGTTTCGCTTTGGGATTTCTAGGTAAACATTCCTCTT 190  
b 121 AACCATGTCACAGCTATCTAAGTTTCGCTTTGGGATTTCTAGGTAAACATTCCTCTT 180  
y 191 CGTGTGCTTTCTGGACACTACCAACATTTATAGAGTTTGTAGAGAGAGAGATCAACCGA 250  
b 181 CGTGTGCTTTCTGGACACTACCAACATTTATAGAGTTTGTAGAGAGAGATCAACCGA 240

RESULT 7  
LOCUS BF068522 389 bp mRNA linear EST 06-DEC-2001  
DEFINITION st83b03.y1 Gm-cl054 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl054-845 5' similar to TR:P93332 P93332 MTN3 GENE PRECURSOR. ; mRNA sequence.  
ACCESSION BF068522.1 GI:10845385  
VERSION EST.  
KEYWORDS Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
1 (bases 1 to 389)  
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Waller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
Public Soybean EST Project  
Unpublished  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Fax: 314 286 1810  
Email: est@wateon.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com  
Insert Length: 1390 Std Error: 0.00  
High quality sequence stop: 346.  
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1. .389  
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/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl054-845"  
/tissue\_type="Leaf, 3 week old, greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl054"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The Harosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from leaf tissue at various developmental stages of 3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

BASE COUNT 106 a 89 c 73 g 120 t 1 others  
ORIGIN  
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Best Local Similarity 88.0%; Pred. No. 1.1e-38;  
Matches 206; Conservative 0; Mismatches 26; Indels 2; Gaps 1;

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Db 2 CAGAAATTAAGCTAGAGCTTCATAGTTCTTCTTTCTACCTCCTCTCTCCCTT 61  
Qy 79 CAGACAAAGGACAAAATC-NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 136  
Db 62 CAGACAAAGGACAAAATCAGTGTGTGAGAGAGAGAGAGAGAAATTCRAAACCT 121  
Qy 137 GTCCACAGTCATCTAAGTTTCGCTTTGGGATTTCTAGGTAAACATTCCTCTCTGTG 196  
Db 122 GTCCACAGTCATCTAAGTTTCGCTTTGGGATTTCTAGGTAAACATTCCTCTCTGTG 181  
Qy 197 CTTTCTGGCACACTACCAACATTTATAGAGTTTGTAGAGAGAGATCAACCGA 250  
Db 182 CTTTCTGGCACACTACCAACATTTATAGAGTTTGTAGAGAGAGATCAACCGA 235

RESULT 8  
LOCUS BG041196 457 bp mRNA linear EST 06-DEC-2001  
DEFINITION sv31a02.y1 Gm-cl057 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl057-1155 5' similar to TR:O82587 O82587 MTN3 HOMOLOG. ; mRNA sequence.  
ACCESSION BG041196  
VERSION BG041196.1 GI:12486992  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
1 (bases 1 to 457)  
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna













GenCore version 5.1.6  
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19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*  
29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg.in.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rod.\*  
36: em.htg.man.\*  
37: em.htg.vrt.\*  
38: em.sy.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	36	14.3	77433	2	AC015736	AC015736 Homo sapi
2	36	14.3	211452	2	AP002010	AP002010 Homo sapi
3	36	14.3	249307	2	AC095208	AC095208 Rattus no
4	35	13.9	68973	2	AC090920	AC090920 Homo sapi
5	35	13.9	69702	2	AC027743	AC027743 Homo sapi
6	35	13.9	70125	2	AC087705	AC087705 Homo sapi
7	35	13.9	136479	2	AC144333	AC144333 Macaca mu
8	35	13.9	140055	2	AP005013	AP005013 Homo sapi
9	35	13.9	158231	2	AC093306	AC093306 Homo sapi
10	35	13.9	160191	2	AC124963	AC124963 Medicago
11	35	13.9	178521	2	AC126450	AC126450 Mus muscu
12	35	13.9	185479	2	AP001484	AP001484 Homo sapi
13	35	13.9	230154	2	AC140686	AC140686 Rattus no
14	35	13.9	236385	2	AC094936	AC094936 Rattus no
15	35	13.9	241607	2	AC113636	AC113636 Rattus no
16	35	13.9	281605	2	AC095329	AC095329 Rattus no
17	34	13.5	45794	2	AC015492	AC015492 Homo sapi
18	34	13.5	52271	2	AC137720	AC137720 Homo sapi
19	34	13.5	61577	2	AC083754	AC083754 Homo sapi
20	34	13.5	62157	2	AC084304	AC084304 Homo sapi
21	34	13.5	64668	2	AC101190	AC101190 Mus muscu
22	34	13.5	64836	2	AC100068	AC100068 Mus muscu
23	34	13.5	65557	2	AC106855	AC106855 Homo sapi
24	34	13.5	65594	2	AC101226	AC101226 Mus muscu
25	34	13.5	66301	2	AC090550	AC090550 Homo sapi
26	34	13.5	67690	2	AC123781	AC123781 Homo sapi
27	34	13.5	68171	2	AC100157	AC100157 Mus muscu
28	34	13.5	108913	2	AC025024	AC025024 Homo sapi
29	34	13.5	110000	2	AC108345	AC108345 Rattus no
30	34	13.5	110000	2	AC141815_1	Continuation (2 of
31	34	13.5	113851	2	AP000571	AP000571 Homo sapi
32	34	13.5	118929	2	AC025976	AC025976 Homo sapi
33	34	13.5	119714	2	AC073028	AC073028 Homo sapi
34	34	13.5	132605	2	AC023450	AC023450 Homo sapi
35	34	13.5	164208	2	AC133383	AC133383 Rattus no
36	34	13.5	165147	2	AC021342	AC021342 Homo sapi
37	34	13.5	180171	2	AC119771	AC119771 Rattus no
38	34	13.5	181504	2	AP001100	AP001100 Homo sapi
39	34	13.5	182295	2	AP001501	AP001501 Homo sapi
40	34	13.5	187411	2	AC115565	AC115565 Rattus no
41	34	13.5	201427	2	AC127843	AC127843 Rattus no
42	34	13.5	204563	2	AC115257	AC115257 Rattus no
43	34	13.5	213666	2	AC020837	AC020837 Mus muscu
44	34	13.5	212276	2	AC098215	AC098215 Rattus no
45	34	13.5	221389	2	AC112122	AC112122 Rattus no
46	34	13.5	222692	2	AC123450	AC123450 Rattus no
47	34	13.5	229363	2	AC094940	AC094940 Rattus no
48	34	13.5	234676	2	AC127042	AC127042 Rattus no
49	34	13.5	237805	2	AC097746	AC097746 Rattus no
50	34	13.5	239944	2	AC134274	AC134274 Rattus no
51	34	13.5	244650	2	AC106532	AC106532 Rattus no
52	34	13.5	244713	2	AC098351	AC098351 Rattus no
53	34	13.5	250480	2	AC115644	AC115644 Rattus no
54	34	13.5	250491	2	AC097760	AC097760 Rattus no
55	34	13.5	251720	2	AC094479	AC094479 Rattus no
56	34	13.5	255530	2	AC118802	AC118802 Rattus no
57	34	13.5	257518	2	AC118524	AC118524 Rattus no
58	34	13.5	259220	2	AC125727	AC125727 Rattus no
59	34	13.5	259783	2	AC111985	AC111985 Rattus no
60	34	13.5	266038	2	AC128025	AC128025 Rattus no
61	34	13.5	307979	2	AC095234	AC095234 Rattus no
62	33	13.1	1521	8	AF382747	AF382747 Cavendish
63	33	13.1	2585	8	AF142683	AF142683 Baphia ma
64	33	13.1	12269	3	AF374374	AF374374 Oikopleur
65	33	13.1	25837	2	AC087198	AC087198 Homo sapi

C 66	33	13.1	29359	2	AP001083	Homo sapi	139	33	13.1	88037	2	PFMAL13P8	AL096782	Plasmodiu
C 67	33	13.1	29716	2	AC103823	Homo sapi	140	33	13.1	89376	2	AC139073	AC139073	Homo sapi
C 68	33	13.1	3240	2	CBH40008	293095 Caenorhabdi	141	33	13.1	91334	2	AC024691	AC024691	Homo sapi
C 69	33	13.1	35692	2	AC067862	Homo sapi	C 142	33	13.1	94153	2	AC139443	AC139443	Rattus no
C 70	33	13.1	44437	2	AC100102	Mus muscu	C 143	33	13.1	99305	2	AC120578	Continuation (4 of	
C 71	33	13.1	44876	2	AC100114	Mus muscu	C 144	33	13.1	100392	2	AP002737	AP002737	Homo sapi
C 72	33	13.1	45050	2	AC100277	Mus muscu	C 145	33	13.1	103408	2	AL606524	AL606524	Homo sapi
C 73	33	13.1	45633	2	AC011630	Homo sapi	C 146	33	13.1	105469	2	AC138215	AC138215	Homo sapi
C 74	33	13.1	47269	2	AC068834	Homo sapi	C 147	33	13.1	105791	2	AC095467	AC095467	Homo sapi
C 75	33	13.1	47436	2	AC106032	Homo sapi	C 148	33	13.1	107448	2	DMBR41K5	AC121843	Drosophil
C 76	33	13.1	49738	2	AC015752	Homo sapi	C 149	33	13.1	108821	2	AC138182	AC138182	Homo sapi
C 77	33	13.1	50531	2	AC100970	Mus muscu	C 150	33	13.1	109097	2	AC013377	AC013377	Homo sapi
C 78	33	13.1	50551	2	AC101140	Mus muscu	C 151	33	13.1	110000	2	AC098035	Continuation (4 of	
C 79	33	13.1	51531	2	AC115089	Homo sapi	C 152	33	13.1	110000	2	AC107134	Continuation (3 of	
C 80	33	13.1	52375	2	AC087052	Homo sapi	C 153	33	13.1	110000	2	AC111970	Continuation (4 of	
C 81	33	13.1	52453	2	AC116153	Homo sapi	C 154	33	13.1	110000	2	AC112374	Continuation (3 of	
C 82	33	13.1	54099	2	AC079963	Homo sapi	C 155	33	13.1	110000	2	AC114698	Continuation (4 of	
C 83	33	13.1	54634	2	AC132201	Homo sapi	C 156	33	13.1	110000	2	AC125151	Continuation (3 of	
C 84	33	13.1	54958	2	AC103850	Homo sapi	C 157	33	13.1	110000	2	AC126295	Continuation (3 of	
C 85	33	13.1	56448	2	AC101445	AC101445 Ciona sav	C 158	33	13.1	110000	2	AC021644	AC021644	Homo sapi
C 86	33	13.1	56983	2	AC068830	Homo sapi	C 159	33	13.1	110000	2	AC141230	AC141230	Homo sapi
C 87	33	13.1	57175	2	AC100243	Mus muscu	C 160	33	13.1	110000	2	AL359032	Continuation (3 of	
C 88	33	13.1	57335	2	AC115739	Mus muscu	C 161	33	13.1	110720	2	AC138189	AC138189	Mus muscu
C 89	33	13.1	58250	2	AC103690	Homo sapi	C 162	33	13.1	115036	2	AP000444	AP000444	Homo sapi
C 90	33	13.1	58520	2	AC036190	Homo sapi	C 163	33	13.1	118218	2	AP000670	AP000670	Homo sapi
C 91	33	13.1	59369	2	AC115765	Mus muscu	C 164	33	13.1	119419	2	AP000666	AP000666	Homo sapi
C 92	33	13.1	59703	2	AC100704	Mus muscu	C 165	33	13.1	121774	2	AC084059	AC084059	Mus muscu
C 93	33	13.1	59866	2	AC100572	Mus muscu	C 166	33	13.1	124696	2	AP000649	AP000649	Homo sapi
C 94	33	13.1	60540	2	AC100489	Mus muscu	C 167	33	13.1	128915	2	AC068465	AC068465	Homo sapi
C 95	33	13.1	60803	2	AC102309	Mus muscu	C 168	33	13.1	132374	2	AC026503	AC026503	Homo sapi
C 96	33	13.1	61101	2	AC083975	Homo sapi	C 169	33	13.1	132451	2	AC140788	AC140788	Mus muscu
C 97	33	13.1	61352	2	AC099964	Mus muscu	C 170	33	13.1	134237	2	AC126501	AC126501	Rattus no
C 98	33	13.1	61375	2	AC068267	Homo sapi	C 171	33	13.1	134867	2	AC013788	AC013788	Homo sapi
C 99	33	13.1	61502	2	AC015619	Homo sapi	C 172	33	13.1	137309	2	AC138008	AC138008	Oryza sat
C 100	33	13.1	62550	2	AC090460	Homo sapi	C 173	33	13.1	137488	2	AC025401	AC025401	Homo sapi
C 101	33	13.1	63084	2	AC100619	Mus muscu	C 174	33	13.1	140819	2	AC012418	AC012418	Homo sapi
C 102	33	13.1	63125	2	AC134783	Homo sapi	C 175	33	13.1	140954	2	AC141538	AC141538	Rattus no
C 103	33	13.1	63192	2	AC135071	Homo sapi	C 176	33	13.1	141281	2	AC018955	AC018955	Mus muscu
C 104	33	13.1	63349	2	AC102470	Mus muscu	C 177	33	13.1	141710	2	AP006167	AP006167	Oryza sat
C 105	33	13.1	63513	2	AC074061	Homo sapi	C 178	33	13.1	141854	2	AC021595	AC021595	Homo sapi
C 106	33	13.1	64323	2	AC015838	Homo sapi	C 179	33	13.1	143239	2	AP005285	AP005285	Oryza sat
C 107	33	13.1	64958	2	AC090905	Homo sapi	C 180	33	13.1	143680	2	AC136539	AC136539	Rattus no
C 108	33	13.1	64970	2	AC099958	Mus muscu	C 181	33	13.1	144037	2	RN141K6	AL603724	Rattus no
C 109	33	13.1	65300	2	AC134677	Homo sapi	C 182	33	13.1	145089	2	AC027093	AC027093	Homo sapi
C 110	33	13.1	65762	2	AC079913	Homo sapi	C 183	33	13.1	145089	2	AP000809	AP000809	Homo sapi
C 111	33	13.1	66015	2	AC009339	AC009339 Drosophil	C 184	33	13.1	147168	2	AC080067	AC080067	Homo sapi
C 112	33	13.1	67338	2	AC090600	Homo sapi	C 185	33	13.1	147184	2	AC135778	AC135778	Homo sapi
C 113	33	13.1	67440	2	AC084138	Homo sapi	C 186	33	13.1	147489	2	AP001926	AP001926	Homo sapi
C 114	33	13.1	68305	2	AC101607	Mus muscu	C 187	33	13.1	148312	2	AP001886	AP001886	Homo sapi
C 115	33	13.1	68373	2	AC115101	Homo sapi	C 188	33	13.1	148772	2	AC055826	AC055826	Homo sapi
C 116	33	13.1	68882	2	AC101569	Mus muscu	C 189	33	13.1	149856	2	AC021411	AC021411	Homo sapi
C 117	33	13.1	68912	2	AC01508	Mus muscu	C 190	33	13.1	150399	2	AC0215784	AC0215784	Homo sapi
C 118	33	13.1	69770	6	AX647131	Sequence	C 191	33	13.1	151386	2	AC013312	AC013312	Homo sapi
C 119	33	13.1	69843	2	AC025903	Homo sapi	C 192	33	13.1	151552	2	AC023437	AC023437	Homo sapi
C 120	33	13.1	70439	2	AC079291	Homo sapi	C 193	33	13.1	152468	2	AP001584	AP001584	Homo sapi
C 121	33	13.1	70471	2	AC130348	Homo sapi	C 194	33	13.1	152728	2	AC128285	AC128285	Rattus no
C 122	33	13.1	70772	2	AC079977	Homo sapi	C 195	33	13.1	152786	2	AP000878	AP000878	Homo sapi
C 123	33	13.1	71256	2	AC105011	Homo sapi	C 196	33	13.1	154158	2	AL365257	AL365257	Homo sapi
C 124	33	13.1	71824	2	AC015759	Homo sapi	C 197	33	13.1	155194	2	AC025231	AC025231	Homo sapi
C 125	33	13.1	71978	2	AC133371	Rattus no	C 198	33	13.1	155317	2	AC067973	AC067973	Homo sapi
C 126	33	13.1	72757	2	AC025301	AC025301	C 199	33	13.1	155388	2	AC139326	AC139326	Mus muscu
C 127	33	13.1	72807	2	AC023525	Homo sapi	C 200	33	13.1	155600	2	AC134601	AC134601	Mus muscu
C 128	33	13.1	72907	2	AC016010	Homo sapi	C 201	33	13.1	155958	2	AC127424	AC127424	Magnaport
C 129	33	13.1	73521	2	AC101583	Mus muscu	C 202	33	13.1	158125	2	AP002447	AP002447	Homo sapi
C 130	33	13.1	73639	2	AC055834	Homo sapi	C 203	33	13.1	158996	2	AP000791	AP000791	Homo sapi
C 131	33	13.1	73814	2	AC100983	Mus muscu	C 204	33	13.1	159845	2	AL355335	AL355335	Homo sapi
C 132	33	13.1	74387	2	AC102894	Mus muscu	C 205	33	13.1	160111	2	AP000780	AP000780	Homo sapi
C 133	33	13.1	75310	2	AC021505	Homo sapi	C 206	33	13.1	161040	2	AC021912	AC021912	Homo sapi
C 134	33	13.1	76410	2	AC016093	Homo sapi	C 207	33	13.1	161678	2	AC009337	AC009337	Homo sapi
C 135	33	13.1	77656	2	AC138743	Homo sapi	C 208	33	13.1	161740	2	AC084778	AC084778	Homo sapi
C 136	33	13.1	79642	2	AC022719	Homo sapi	C 209	33	13.1	162010	2	AC010824	AC010824	Homo sapi
C 137	33	13.1	81337	2	AC100918	Mus muscu	C 210	33	13.1	163273	2	AC142486	AC142486	Rattus no
C 138	33	13.1	87526	2	AC018485	Drosophil	C 211	33	13.1	164420	2	AC023323	AC023323	Homo sapi

C 212	33	13.1	164655	2	AC080134	AC080134 Homo sapi	285	33	13.1	217203	2	AC139956	AC139956 Rattus no
213	33	13.1	164671	2	AP002401	AP002401 Homo sapi	C 286	33	13.1	218963	2	AC131850	AC131850 Rattus no
214	33	13.1	165581	2	AC016404	AC016404 Homo sapi	287	33	13.1	220507	2	AC098007	AC098007 Rattus no
215	33	13.1	166061	2	AC134876	AC134876 Homo sapi	288	33	13.1	220867	2	AC094006	AC094006 Rattus no
C 216	33	13.1	166895	2	AC023415	AC023415 Homo sapi	C 289	33	13.1	222378	2	AC015862	AC015862 Homo sapi
C 217	33	13.1	166992	2	AC119973	AC119973 Mus muscu	C 290	33	13.1	222477	2	AP001847	AP001847 Homo sapi
C 218	33	13.1	167205	2	AC023871	AC023871 Homo sapi	C 291	33	13.1	223151	2	AC098029	AC098029 Rattus no
C 219	33	13.1	167229	2	AC023799	AC137799 Homo sapi	C 292	33	13.1	224788	2	AP001905	AP001905 Homo sapi
C 220	33	13.1	169236	2	AC022198	AC022198 Homo sapi	C 293	33	13.1	225230	2	AC022235	Mus muscu
C 221	33	13.1	169308	2	AL591000	AL591000 Homo sapi	C 294	33	13.1	229822	2	AC138642	Mus muscu
C 222	33	13.1	169312	2	AC016094	AC016094 Homo sapi	C 295	33	13.1	230620	2	AC109649	Rattus no
C 223	33	13.1	169623	2	AC011158	AC011158 Homo sapi	C 296	33	13.1	230703	2	AC120663	Rattus no
C 224	33	13.1	170788	2	AC139387	AC139387 Rattus no	C 297	33	13.1	231349	2	AC138617	Mus muscu
C 225	33	13.1	170918	2	AC143944	AC143944 Macaca mu	C 298	33	13.1	231698	2	AC118117	Rattus no
C 226	33	13.1	170950	2	AC144050	AC144050 Macaca mu	C 299	33	13.1	233428	2	AC011064	Drosophil
C 227	33	13.1	171006	2	AP002504	AP002504 Homo sapi	C 300	33	13.1	234844	2	AC111734	Rattus no
C 228	33	13.1	172921	2	AP002454	AP002454 Homo sapi	C 301	33	13.1	235151	2	AC125640	Rattus no
C 229	33	13.1	173657	2	AP001014	AP001014 Homo sapi	C 302	33	13.1	235333	2	AC109551	Rattus no
C 230	33	13.1	174203	2	AC141570	AC141570 Rattus no	C 303	33	13.1	236646	2	AC142152	Rattus no
C 231	33	13.1	174280	2	AC011077	AC011077 Homo sapi	C 304	33	13.1	240262	2	AC137467	Rattus no
C 232	33	13.1	174327	2	AL672191	AL672191 Homo sapi	C 305	33	13.1	240396	2	AC138343	Mus muscu
C 233	33	13.1	174383	2	AC012053	AC012053 Homo sapi	C 306	33	13.1	241730	2	AC103283	Rattus no
C 234	33	13.1	174894	2	AC123915	AC123915 Mus muscu	C 307	33	13.1	243915	2	AC117981	Rattus no
C 235	33	13.1	175980	2	AC025082	AC025082 Homo sapi	C 308	33	13.1	243887	2	AC024898	Homo sapi
C 236	33	13.1	176331	2	AL831747	AL831747 Danio rer	C 309	33	13.1	244010	2	AC105848	Rattus no
C 237	33	13.1	176578	2	AC041008	AC041008 Homo sapi	C 310	33	13.1	244224	2	AC125992	Rattus no
C 238	33	13.1	177443	2	AP001164	AP001164 Homo sapi	C 311	33	13.1	244477	2	AC131832	Rattus no
C 239	33	13.1	177660	2	AC141656	AC141656 Rattus no	C 312	33	13.1	246083	2	AC106313	Rattus no
C 240	33	13.1	177716	2	AP001027	AP001027 Homo sapi	C 313	33	13.1	246212	2	AC109769	Rattus no
C 241	33	13.1	178478	2	AP002834	AP002834 Homo sapi	C 314	33	13.1	246680	2	AC094910	Rattus no
C 242	33	13.1	179843	2	AP001272	AP001272 Homo sapi	C 315	33	13.1	252370	2	AC117214	Mus muscu
C 243	33	13.1	180273	2	AP002894	AP002894 Homo sapi	C 316	33	13.1	252825	2	AC132024	Rattus no
C 244	33	13.1	180291	2	AC020711	AC020711 Homo sapi	C 317	33	13.1	253176	2	AC094477	Rattus no
C 245	33	13.1	180354	2	AC009689	AC009689 Homo sapi	C 318	33	13.1	253787	2	AC130832	Mus muscu
C 246	33	13.1	180962	2	AC068917	AC068917 Homo sapi	C 319	33	13.1	256093	2	AC105672	Rattus no
C 247	33	13.1	181254	2	AP000825	AP000825 Homo sapi	C 320	33	13.1	256473	2	AC109689	Rattus no
C 248	33	13.1	181360	2	AC132844	AC132844 Mus muscu	C 321	33	13.1	256528	2	AC108270	Rattus no
C 249	33	13.1	181515	2	AC119068	AC119068 Canis fam	C 322	33	13.1	257178	2	AC114088	Rattus no
C 250	33	13.1	181805	2	AC114445	AC114445 Rattus no	C 323	33	13.1	258520	2	AC135085	Mus muscu
C 251	33	13.1	182928	2	AP001161	AP001161 Homo sapi	C 324	33	13.1	263352	2	AC095748	Rattus no
C 252	33	13.1	184513	2	AC024433	AC024433 Homo sapi	C 325	33	13.1	266617	2	AC124879	Rattus no
C 253	33	13.1	185195	2	AC074001	AC074001 Homo sapi	C 326	33	13.1	267137	2	AC098319	Rattus no
C 254	33	13.1	185644	2	AL391723	AL391723 Homo sapi	C 327	33	13.1	270567	2	AC138086	Homo sapi
C 255	33	13.1	187214	2	AC121384	AC121384 Rattus no	C 328	33	13.1	270706	2	AC129862	Rattus no
C 256	33	13.1	188088	2	AC137982	AC137982 Mus muscu	C 329	33	13.1	271496	2	AC142073	Rattus no
C 257	33	13.1	188514	2	AC104554	AC104554 Mus muscu	C 330	33	13.1	272226	2	AC105691	Rattus no
C 258	33	13.1	188565	2	AC125250	AC125250 Mus muscu	C 331	33	13.1	278521	2	AC092715	Homo sapi
C 259	33	13.1	189623	2	AC1018640	AC1018640 Homo sapi	C 332	33	13.1	285107	2	AC103104	Rattus no
C 260	33	13.1	190105	2	AC140255	AC140255 Mus muscu	C 333	33	13.1	292173	2	BX294381	Danio rer
C 261	33	13.1	190886	2	AC125079	AC125079 Mus muscu	C 334	33	13.1	301662	2	AC127291	Mus muscu
C 262	33	13.1	191020	2	AC090758	AC090758 Homo sapi	C 335	33	13.1	310448	2	AC131354	Rattus no
C 263	33	13.1	191196	2	AL441903	AL441903 Homo sapi	C 336	33	13.1	318589	2	AC120476	Rattus no
C 264	33	13.1	191564	2	AC139653	AC139653 Rattus no	C 337	33	13.1	319335	2	AC106226	Rattus no
C 265	33	13.1	193433	2	AP001523	AP001523 Homo sapi	C 338	33	13.1	323417	2	AC109609	Rattus no
C 266	33	13.1	193787	2	AP000774	AP000774 Homo sapi	C 339	33	13.1	327654	2	AC020816	Mus muscu
C 267	33	13.1	195029	2	AC007902	AC007902 Homo sapi	C 340	33	13.1	329577	2	AC128988	Rattus no
C 268	33	13.1	195419	2	AP005132	AP005132 Homo sapi	C 341	33	13.1	338462	2	BX465196	Mus muscu
C 269	33	13.1	196252	2	BX324145	BX324145 Danio rer	C 342	33	13.1	342774	2	AC116082	Rattus no
C 270	33	13.1	196511	2	AP000854	AP000854 Homo sapi	C 343	33	13.1	348465	2	AC131165	Rattus no
C 271	33	13.1	196933	2	AC079854	AC079854 Homo sapi	C 344	32	12.7	263	11	GA1076	Cl4M20 Plas
C 272	33	13.1	197295	2	AC139652	AC139652 Rattus no	C 345	32	12.7	735	8	AY101159	Cordisepa
C 273	33	13.1	197866	2	AC068293	AC068293 Homo sapi	C 346	32	12.7	10835	8	AY146811	Zea mays
C 274	33	13.1	198136	2	AC090165	AC090165 Homo sapi	C 347	32	12.7	23489	2	AC091079	Homo sapi
C 275	33	13.1	200000	2	AC004618	AC004618 Homo sapi	C 348	32	12.7	32926	2	AL354742	Homo sapi
C 276	33	13.1	200135	2	AC121046	AC121046 Rattus no	C 349	32	12.7	35284	2	CEH27501	Caenorhabdi
C 277	33	13.1	202217	2	AC116730	AC116730 Mus muscu	C 350	32	12.7	36608	2	AC104227	Homo sapi
C 278	33	13.1	208497	2	AC127844	AC127844 Rattus no	C 351	32	12.7	38360	2	AC087400	Homo sapi
C 279	33	13.1	208657	2	AC046179	AC046179 Homo sapi	C 352	32	12.7	38428	2	AC145166	Homo sapi
C 280	33	13.1	210147	2	BX294157	BX294157 Danio rer	C 353	32	12.7	43295	2	AC024381	Homo sapi
C 281	33	13.1	210876	2	AC098466	AC098466 Rattus no	C 354	32	12.7	43963	2	AC104243	Homo sapi
C 282	33	13.1	212309	2	AC141534	AC141534 Rattus no	C 355	32	12.7	44433	2	AC110052	Homo sapi
C 283	33	13.1	215201	2	BX294007	BX294007 Mus muscu	C 356	32	12.7	44465	2	AC025007	Homo sapi
C 284	33	13.1	215315	2	AC107671	AC107671 Mus muscu	C 357	32	12.7	44693	2	AC087338	Homo sapi



358	32	12.7	47483	2	AC141834	AC141834	Apis mell	C 431	32	12.7	67951	2	AC102112	AC102112	Mus muscu
359	32	12.7	47760	6	AX059454	AX059454	Sequence	C 432	32	12.7	67984	2	AC118190	AC118190	Mus muscu
360	32	12.7	48864	2	AC060774	AC060774	Homo sapi	C 433	32	12.7	68074	2	AC101494	AC101494	Mus muscu
361	32	12.7	49688	2	AC090162	AC090162	Homo sapi	C 434	32	12.7	68087	2	AC023856	AC023856	Homo sapi
362	32	12.7	50994	2	AC104591	AC104591	Homo sapi	C 435	32	12.7	68326	2	AC055793	AC055793	Mus muscu
363	32	12.7	51896	2	AC068031	AC068031	Homo sapi	C 436	32	12.7	68407	2	AC048372	AC048372	Homo sapi
364	32	12.7	52226	2	AC107902	AC107902	Homo sapi	C 437	32	12.7	68445	2	AC124257	AC124257	Homo sapi
365	32	12.7	52915	2	AC127531	AC127531	Homo sapi	C 438	32	12.7	68451	2	AC110061	AC110061	Homo sapi
366	32	12.7	53735	2	AC101365	AC101365	Mus muscu	C 439	32	12.7	68630	2	AC090468	AC090468	Homo sapi
367	32	12.7	54188	2	AC100937	AC100937	Mus muscu	C 440	32	12.7	68999	2	AC100684	AC100684	Mus muscu
368	32	12.7	54296	2	AC119232	AC119232	Mus muscu	C 441	32	12.7	69161	2	AC101153	AC101153	Mus muscu
369	32	12.7	54606	2	AC100097	AC100097	Mus muscu	C 442	32	12.7	69337	2	AC101261	AC101261	Mus muscu
370	32	12.7	55496	2	AC100480	AC100480	Mus muscu	C 443	32	12.7	69354	2	AC069342	AC069342	Homo sapi
371	32	12.7	55772	2	AC114339	AC114339	Homo sapi	C 444	32	12.7	70183	2	AC090566	AC090566	Homo sapi
372	32	12.7	55956	2	AC101559	AC101559	Mus muscu	C 445	32	12.7	70282	2	AC111072	AC111072	Mus muscu
373	32	12.7	56213	2	AC106023	AC106023	Mus muscu	C 446	32	12.7	70508	2	AC1016784	AC1016784	Homo sapi
374	32	12.7	56264	2	AC100886	AC100886	Mus muscu	C 447	32	12.7	70589	2	AC087515	AC087515	Homo sapi
375	32	12.7	56690	2	AC100882	AC100882	Mus muscu	C 448	32	12.7	70751	2	AC101724	AC101724	Mus muscu
376	32	12.7	57286	2	AC117683	AC117683	Mus muscu	C 449	32	12.7	70798	2	AC024273	AC024273	Homo sapi
377	32	12.7	57865	2	AC101541	AC101541	Ciona sav	C 450	32	12.7	70864	2	AC101195	AC101195	Mus muscu
378	32	12.7	58496	2	AC101077	AC101077	Mus muscu	C 451	32	12.7	71063	2	AC027580	AC027580	Homo sapi
379	32	12.7	58569	2	AC134424	AC134424	Homo sapi	C 452	32	12.7	71353	2	AC135175	AC135175	Homo sapi
380	32	12.7	58657	2	AC101030	AC101030	Mus muscu	C 453	32	12.7	71491	2	AC124619	AC124619	Mus muscu
381	32	12.7	59008	2	AC100379	AC100379	Mus muscu	C 454	32	12.7	71496	2	AC090722	AC090722	Homo sapi
382	32	12.7	59199	2	AC132848	AC132848	Mus muscu	C 455	32	12.7	71508	2	AC101219	AC101219	Mus muscu
383	32	12.7	59413	2	AC136535	AC136535	Rattus no	C 456	32	12.7	71662	2	AC027786	AC027786	Homo sapi
384	32	12.7	59445	2	AC099952	AC099952	Mus muscu	C 457	32	12.7	71704	2	AC068468	AC068468	Homo sapi
385	32	12.7	59747	2	AC069053	AC069053	Homo sapi	C 458	32	12.7	71920	2	AC105200	AC105200	Homo sapi
386	32	12.7	59806	2	AC101192	AC101192	Mus muscu	C 459	32	12.7	71979	2	AC101186	AC101186	Mus muscu
387	32	12.7	60211	2	AC068685	AC068685	Homo sapi	C 460	32	12.7	72005	2	AC067776	AC067776	Homo sapi
388	32	12.7	61143	2	AC099802	AC099802	Homo sapi	C 461	32	12.7	72757	2	AC025301	AC025301	Homo sapi
389	32	12.7	61325	2	AC100109	AC100109	Mus muscu	C 462	32	12.7	72784	2	AC100279	AC100279	Mus muscu
390	32	12.7	61451	2	AC101514	AC101514	Mus muscu	C 463	32	12.7	73322	2	AC069380	AC069380	Homo sapi
391	32	12.7	61469	2	AC107910	AC107910	Homo sapi	C 464	32	12.7	73472	2	AC084770	AC084770	Homo sapi
392	32	12.7	61956	2	AC101376	AC101376	Mus muscu	C 465	32	12.7	73516	2	AC100369	AC100369	Mus muscu
393	32	12.7	62125	2	AC137958	AC137958	Mus muscu	C 466	32	12.7	73539	2	AC129493	AC129493	Homo sapi
394	32	12.7	62186	2	AC110604	AC110604	Homo sapi	C 467	32	12.7	73555	2	AC021278	AC021278	Homo sapi
395	32	12.7	62512	2	AC103999	AC103999	Homo sapi	C 468	32	12.7	73638	2	AC015613	AC015613	Homo sapi
396	32	12.7	62859	2	AC101719	AC101719	Mus muscu	C 469	32	12.7	73789	2	AC101587	AC101587	Mus muscu
397	32	12.7	62861	2	AC137726	AC137726	Homo sapi	C 470	32	12.7	74206	2	AC100080	AC100080	Mus muscu
398	32	12.7	63063	2	AC099996	AC099996	Mus muscu	C 471	32	12.7	75035	2	AC069096	AC069096	Homo sapi
399	32	12.7	63369	2	AC100861	AC100861	Homo sapi	C 472	32	12.7	75326	2	AC026999	AC026999	Homo sapi
400	32	12.7	63599	2	AC116159	AC116159	Homo sapi	C 473	32	12.7	75594	2	AC021273	AC021273	Homo sapi
401	32	12.7	63753	2	AC090089	AC090089	Homo sapi	C 474	32	12.7	76089	2	AC026945	AC026945	Homo sapi
402	32	12.7	63910	2	AC135341	AC135341	Homo sapi	C 475	32	12.7	76410	2	AC016093	AC016093	Homo sapi
403	32	12.7	63966	2	AC083929	AC083929	Homo sapi	C 476	32	12.7	76442	2	AC138234	AC138234	Mus muscu
404	32	12.7	64303	2	AC103754	AC103754	Homo sapi	C 477	32	12.7	76856	2	AC142858	AC142858	Continuation (4 of
405	32	12.7	64439	2	AC120872	AC120872	Mus muscu	C 478	32	12.7	77096	2	AC016283	AC016283	Homo sapi
406	32	12.7	64536	2	AC135067	AC135067	Homo sapi	C 479	32	12.7	78011	2	AC016362	AC016362	Homo sapi
407	32	12.7	64611	2	AC115702	AC115702	Mus muscu	C 480	32	12.7	79338	2	AC025399	AC025399	Mus muscu
408	32	12.7	64676	2	AC136335	AC136335	Homo sapi	C 481	32	12.7	79937	2	AC025399	AC025399	Homo sapi
409	32	12.7	64803	2	AC091149	AC091149	Homo sapi	C 482	32	12.7	80053	2	AC022617	AC022617	Homo sapi
410	32	12.7	64869	2	AC125429	AC125429	Homo sapi	C 483	32	12.7	80318	2	AC016300	AC016300	Homo sapi
411	32	12.7	64962	2	AC124644	AC124644	Mus muscu	C 484	32	12.7	80866	2	AC012649	AC012649	Drosophil
412	32	12.7	65031	2	AC114338	AC114338	Mus muscu	C 485	32	12.7	80909	2	AC016842	AC016842	Homo sapi
413	32	12.7	65128	2	AC104210	AC104210	Homo sapi	C 486	32	12.7	81436	2	AC023552	AC023552	Homo sapi
414	32	12.7	65273	2	AC120357	AC120357	Mus muscu	C 487	32	12.7	81448	2	AC026630	AC026630	Homo sapi
415	32	12.7	65459	2	AC100135	AC100135	Mus muscu	C 488	32	12.7	81675	2	AC016354	AC016354	Homo sapi
416	32	12.7	65512	2	AC101322	AC101322	Mus muscu	C 489	32	12.7	82023	2	AC100843	AC100843	Mus muscu
417	32	12.7	65550	2	AC011923	AC011923	Homo sapi	C 490	32	12.7	82356	2	AC144912	AC144912	Mus muscu
418	32	12.7	65767	2	AC015704	AC015704	Homo sapi	C 491	32	12.7	82665	2	AC023204	AC023204	Homo sapi
419	32	12.7	65973	2	AC102332	AC102332	Mus muscu	C 492	32	12.7	82837	2	AC022590	AC022590	Homo sapi
420	32	12.7	66137	2	AC101526	AC101526	Mus muscu	C 493	32	12.7	84483	2	AC021936	AC021936	Homo sapi
421	32	12.7	66308	2	AC100618	AC100618	Mus muscu	C 494	32	12.7	84581	2	AC024546	AC024546	Homo sapi
422	32	12.7	66393	2	AC100424	AC100424	Mus muscu	C 495	32	12.7	85012	2	AC133713	AC133713	Rattus no
423	32	12.7	66639	2	AC068932	AC068932	Homo sapi	C 496	32	12.7	85049	2	AC137945	AC137945	Mus muscu
424	32	12.7	66686	2	AC087669	AC087669	Homo sapi	C 497	32	12.7	86455	2	AC126295	AC126295	Continuation (5 of
425	32	12.7	66985	2	AC127516	AC127516	Homo sapi	C 498	32	12.7	87141	2	AC020662	AC020662	Homo sapi
426	32	12.7	67179	2	AC083972	AC083972	Homo sapi	C 499	32	12.7	87147	2	AC107496	AC107496	Continuation (5 of
427	32	12.7	67224	2	AC129953	AC129953	Bos tauru	C 500	32	12.7	88940	2	AC138602	AC138602	Mus muscu
428	32	12.7	67711	2	AC090353	AC090353	Homo sapi	C 501	32	12.7	90597	2	AC142520	AC142520	Rattus no
429	32	12.7	67713	2	AC102796	AC102796	Homo sapi	C 502	32	12.7	92141	2	AC021565	AC021565	Homo sapi
430	32	12.7	67763	2	AC103752	AC103752	Homo sapi	C 503	32	12.7	92315	2	AC101653	AC101653	Mus muscu

504	32	12.7	92636	2	AC022747	Homo sapi	AC022747 Homo sapi
505	32	12.7	93121	2	DMBR48A1	Drosophila	AL121844 Drosophila
506	32	12.7	95208	2	AC115769	Mus muscu	AC115769 Mus muscu
507	32	12.7	95271	2	AL450383	Homo sapi	AL450383 Homo sapi
508	32	12.7	95689	2	AC117735	Mus muscu	AC117735 Mus muscu
509	32	12.7	95751	2	AC119650.3	Continuation (4 of	Continuation (4 of
510	32	12.7	96798	2	AC138698	Homo sapi	AC138698 Homo sapi
511	32	12.7	96895	2	AC141768	Apis mell	AC141768 Apis mell
512	32	12.7	96895	2	AC141768	Apis mell	AC141768 Apis mell
513	32	12.7	97021	2	AC138255	Mus muscu	AC138255 Mus muscu
514	32	12.7	104494	2	AC012166	Drosophila	AC012166 Drosophila
515	32	12.7	105011	2	AC096724	Homo sapi	AC096724 Homo sapi
516	32	12.7	107007	2	AC142685	Macaca mu	AC142685 Macaca mu
517	32	12.7	107304	2	AC016274	Homo sapi	AC016274 Homo sapi
518	32	12.7	110000	2	AC009801	Homo sapi	AC009801 Homo sapi
519	32	12.7	110000	2	AC091343.5	Continuation (6 of	Continuation (6 of
520	32	12.7	110000	2	AC091343.5	Continuation (9 of	Continuation (9 of
521	32	12.7	110000	2	AC095863.08	Rattus no	AC097780 Rattus no
522	32	12.7	110000	2	AC098036.1	Continuation (2 of	Continuation (2 of
523	32	12.7	110000	2	AC106415.2	Continuation (3 of	Continuation (3 of
524	32	12.7	110000	2	AC112563.3	Continuation (4 of	Continuation (4 of
525	32	12.7	110000	2	AC115386.1	Continuation (2 of	Continuation (2 of
526	32	12.7	110000	2	AC018724	Homo sapi	AC140288 Mus muscu
527	32	12.7	110000	2	AC140288.0	Continuation (2 of	Continuation (2 of
528	32	12.7	110000	2	AC140288.1	Continuation (2 of	Continuation (2 of
529	32	12.7	110000	2	AC141230.0	Homo sapi	AC141230 Homo sapi
530	32	12.7	110000	2	AC142976	Macaca mu	AC142976 Macaca mu
531	32	12.7	110000	2	AL831785.5	Continuation (6 of	Continuation (6 of
532	32	12.7	110000	2	AL831785.5	Continuation (13 of	Continuation (13 of
533	32	12.7	110000	2	AL929091.12	Continuation (8 of	Continuation (8 of
534	32	12.7	117710	2	AC111053	Mus muscu	AC111053 Mus muscu
535	32	12.7	120316	2	AC025984	Homo sapi	AC025984 Homo sapi
536	32	12.7	125150	2	AC005450	Drosophila	AC005450 Drosophila
537	32	12.7	127362	2	AC010014	Drosophila	AC010014 Drosophila
538	32	12.7	127372	2	AC068172	Mus muscu	AC068172 Mus muscu
539	32	12.7	127373	2	AC013330	Homo sapi	AC013330 Homo sapi
540	32	12.7	127505	2	AC061980	Homo sapi	AC061980 Homo sapi
541	32	12.7	128465	2	AC138569	Gallus ga	AC138569 Gallus ga
542	32	12.7	128561	2	AC068729	Homo sapi	AC068729 Homo sapi
543	32	12.7	128822	2	AP001260	Homo sapi	AP001260 Homo sapi
544	32	12.7	129218	2	AC138851	Homo sapi	AC138851 Homo sapi
545	32	12.7	129451	2	AC073783	Mus muscu	AC073783 Mus muscu
546	32	12.7	129755	2	AC019296	Homo sapi	AC019296 Homo sapi
547	32	12.7	131298	2	AC142959	Macaca mu	AC142959 Macaca mu
548	32	12.7	131694	2	AC009619	Homo sapi	AC009619 Homo sapi
549	32	12.7	132270	2	AC141705	Apis mell	AC141705 Apis mell
550	32	12.7	132290	2	AC026137	Homo sapi	AC026137 Homo sapi
551	32	12.7	133273	2	AC068586	Homo sapi	AC068586 Homo sapi
552	32	12.7	133622	2	AC141813	Apis mell	AC141813 Apis mell
553	32	12.7	133997	2	AC015469	Homo sapi	AC015469 Homo sapi
554	32	12.7	134940	2	AC018939	Homo sapi	AC018939 Homo sapi
555	32	12.7	135321	2	AC142021	Rattus no	AC142021 Rattus no
556	32	12.7	136212	2	AC139386	Rattus no	AC139386 Rattus no
557	32	12.7	136448	2	AC012231	Homo sapi	AC012231 Homo sapi
558	32	12.7	136869	2	AP005193	Oryza sat	AP005193 Oryza sat
559	32	12.7	137911	2	AC009769	Homo sapi	AC009769 Homo sapi
560	32	12.7	138295	2	AC024448	Homo sapi	AC024448 Homo sapi
561	32	12.7	140897	2	AC143170	Macaca mu	AC143170 Macaca mu
562	32	12.7	141529	2	AC025330	Homo sapi	AC025330 Homo sapi
563	32	12.7	142126	2	AC026139	Homo sapi	AC026139 Homo sapi
564	32	12.7	142781	2	AC141934	Rattus no	AC141934 Rattus no
565	32	12.7	142986	2	AC023467	Homo sapi	AC023467 Homo sapi
566	32	12.7	143409	2	AP001787	Homo sapi	AP001787 Homo sapi
567	32	12.7	144888	2	AC023895	Homo sapi	AC023895 Homo sapi
568	32	12.7	146814	2	AC022320	Homo sapi	AC022320 Homo sapi
569	32	12.7	149269	2	AC008690	Homo sapi	AC008690 Homo sapi
570	32	12.7	150207	2	AL451067	Homo sapi	AL451067 Homo sapi
571	32	12.7	150477	2	AC024441	Homo sapi	AC024441 Homo sapi
572	32	12.7	152141	2	AC090189	Homo sapi	AC090189 Homo sapi
573	32	12.7	152575	2	AC141690	Apis mell	AC141690 Apis mell
574	32	12.7	153469	2	AC130528	Mus muscu	AC130528 Mus muscu
575	32	12.7	153833	2	AP001996	Homo sapi	AP001996 Homo sapi
576	32	12.7	157953	2	AC141134	Rattus no	AC141134 Rattus no
577	32	12.7	158229	2	AC021363	Homo sapi	AC021363 Homo sapi
578	32	12.7	159299	2	AC114713	Rattus no	AC114713 Rattus no
579	32	12.7	160699	2	AC140157	Canis fam	AC140157 Canis fam
580	32	12.7	160737	2	AC138731	Pongo pyg	AC138731 Pongo pyg
581	32	12.7	162493	2	AC026213	Homo sapi	AC026213 Homo sapi
582	32	12.7	162493	2	AC073972	Homo sapi	AC073972 Homo sapi
583	32	12.7	162508	2	AC025870	Homo sapi	AC025870 Homo sapi
584	32	12.7	162606	2	AC016348	Homo sapi	AC016348 Homo sapi
585	32	12.7	163551	2	AC015777	Homo sapi	AC015777 Homo sapi
586	32	12.7	163916	2	AP002413	Homo sapi	AP002413 Homo sapi
587	32	12.7	164159	2	AC100853	Homo sapi	AC100853 Homo sapi
588	32	12.7	164297	2	AC012138	Homo sapi	AC012138 Homo sapi
589	32	12.7	164396	2	AC024961	Homo sapi	AC024961 Homo sapi
590	32	12.7	164473	2	AP001108	Homo sapi	AP001108 Homo sapi
591	32	12.7	164652	2	AC026923	Homo sapi	AC026923 Homo sapi
592	32	12.7	164846	2	AC023007	Homo sapi	AC023007 Homo sapi
593	32	12.7	164918	2	AC013373	Homo sapi	AC013373 Homo sapi
594	32	12.7	164959	2	AC087823	Homo sapi	AC087823 Homo sapi
595	32	12.7	165278	2	AC027380	Mus muscu	AC027380 Mus muscu
596	32	12.7	165404	2	AC084119	Homo sapi	AC084119 Homo sapi
597	32	12.7	166549	2	AC025990	Homo sapi	AC025990 Homo sapi
598	32	12.7	166689	2	AC058815	Homo sapi	AC058815 Homo sapi
599	32	12.7	167305	2	AL590409	Homo sapi	AL590409 Homo sapi
600	32	12.7	167833	2	AC122742	Mus muscu	AC122742 Mus muscu
601	32	12.7	168081	2	AC083955	Mus muscu	AC083955 Mus muscu
602	32	12.7	168262	2	AC143997	Macaca mu	AC143997 Macaca mu
603	32	12.7	168527	2	AC040993	Homo sapi	AC040993 Homo sapi
604	32	12.7	169328	2	AC016281	Homo sapi	AC016281 Homo sapi
605	32	12.7	169457	2	AC009216	Drosophila	AC009216 Drosophila
606	32	12.7	170393	2	AC024304	Homo sapi	AC024304 Homo sapi
607	32	12.7	170496	2	AC137002	Oryza sat	AC137002 Oryza sat
608	32	12.7	170795	2	AC021346	Homo sapi	AC021346 Homo sapi
609	32	12.7	172346	2	AC016349	Homo sapi	AC016349 Homo sapi
610	32	12.7	172387	2	AC103561	Homo sapi	AC103561 Homo sapi
611	32	12.7	172485	2	AC141978	Rattus no	AC141978 Rattus no
612	32	12.7	172562	2	AC136120	Rattus no	AC136120 Rattus no
613	32	12.7	173340	2	AC015760	Homo sapi	AC015760 Homo sapi
614	32	12.7	173917	2	AC027476	Homo sapi	AC027476 Homo sapi
615	32	12.7	174380	2	AL356116	Homo sapi	AL356116 Homo sapi
616	32	12.7	174393	2	AC126618	Rattus no	AC126618 Rattus no
617	32	12.7	174915	2	AP001390	Homo sapi	AP001390 Homo sapi
618	32	12.7	174937	2	AC022245	Homo sapi	AC022245 Homo sapi
619	32	12.7	175288	2	AC119361	Rattus no	AC119361 Rattus no
620	32	12.7	175288	2	AC023589	Homo sapi	AC023589 Homo sapi
621	32	12.7	175771	2	AC016510	Homo sapi	AC016510 Homo sapi
622	32	12.7	175807	2	AC018663	Mus muscu	AC018663 Mus muscu
623	32	12.7	175977	2	AC058808	Homo sapi	AC058808 Homo sapi
624	32	12.7	176372	2	AC026030	Homo sapi	AC026030 Homo sapi
625	32	12.7	177531	2	AC129120	Rattus no	AC129120 Rattus no
626	32	12.7	177635	2	AC141509	Rattus no	AC141509 Rattus no
627	32	12.7	177680	2	AP001910	Homo sapi	AP001910 Homo sapi
628	32	12.7	178122	2	AC095848	Rattus no	AC095848 Rattus no
629	32	12.7	178384	2	AL591026	Homo sapi	AL591026 Homo sapi
630	32	12.7	178640	2	AC069170	Homo sapi	AC069170 Homo sapi
631	32	12.7	179323	2	AC011852	Homo sapi	AC011852 Homo sapi
632	32	12.7	179845	2	AY178787	Canis fam	AY178787 Canis fam
633	32	12.7	180018	2	AC023417	Homo sapi	AC023417 Homo sapi
634	32	12.7	180044	2	AC026942	Homo sapi	AC026942 Homo sapi
635	32	12.7	181290	2	BX005286	Danio rer	BX005286 Danio rer
636	32	12.7	182673	2	AC073105	Homo sapi	AC073105 Homo sapi
637	32	12.7	182690	2	AC009998	Homo sapi	AC009998 Homo sapi
638	32	12.7	182799	2	AC073526	Homo sapi	AC073526 Homo sapi
639	32	12.7	182990	2	AC125866	Rattus no	AC125866 Rattus no
640	32	12.7	183345	2	AC120550	Mus muscu	AC120550 Mus muscu
641	32	12.7	183350	2	AC102305	Mus muscu	AC102305 Mus muscu
642	32	12.7	184127	2	AC140578	Macaca mu	AC140578 Macaca mu
643	32	12.7	184244	2	AC127328	Homo sapi	AC127328 Homo sapi
644	32	12.7	184342	2	AC127990	Rattus no	AC127990 Rattus no
645	32	12.7	184767	2	AC084363	Homo sapi	AC084363 Homo sapi
646	32	12.7	185272	2	AC121394	Rattus no	AC121394 Rattus no
647	32	12.7	185360	2	AC126230	Bos tauru	AC126230 Bos tauru
648	32	12.7	185440	2	AC015499	Homo sapi	AC015499 Homo sapi
649	32	12.7	185810	2	AC136052	Rattus no	AC136052 Rattus no

C 650	32	12.7	186044	2	AC084099	Homo sapi	723	32	12.7	229916	2	AC132022	AC132022	Rattus no
C 651	32	12.7	186184	2	AC139894	Rattus no	724	32	12.7	230254	2	AC074163	AC074163	Mus muscu
C 652	32	12.7	187038	2	AC021179	Homo sapi	725	32	12.7	230273	2	AC110400	AC110400	Rattus no
C 653	32	12.7	187150	2	AC016282	Homo sapi	C 726	32	12.7	230393	2	AC133303	AC133303	Rattus no
C 654	32	12.7	187557	2	AC074223	Mus muscu	C 727	32	12.7	230787	2	AC103473	AC103473	Rattus no
C 655	32	12.7	188152	2	AC025847	Homo sapi	C 728	32	12.7	230877	2	AC105583	AC105583	Rattus no
C 656	32	12.7	188540	2	AC011108	Homo sapi	729	32	12.7	231772	2	AC124926	AC124926	Rattus no
C 657	32	12.7	191109	2	AC137370	Rattus no	730	32	12.7	232244	2	AC114524	AC114524	Rattus no
C 658	32	12.7	192142	2	AC136061	Rattus no	731	32	12.7	232792	2	AC106657	AC106657	Rattus no
C 659	32	12.7	192372	2	AC134754	Rattus no	C 732	32	12.7	233247	2	AC134936	AC134936	Rattus no
C 660	32	12.7	193001	2	AC023231	Homo sapi	C 733	32	12.7	233363	2	AC078919	AC078919	Homo sapi
C 661	32	12.7	193001	2	AC023231	Homo sapi	C 734	32	12.7	233380	2	AC133857	AC133857	Rattus no
C 662	32	12.7	194247	2	AC128533	Rattus no	C 735	32	12.7	234213	2	BX510954	BX510954	Danio rer
C 663	32	12.7	194328	2	AC139802	Rattus no	C 736	32	12.7	235554	2	AC118332	AC118332	Rattus no
C 664	32	12.7	195506	2	AC015796	Mus muscu	C 737	32	12.7	235662	2	AC126709	AC126709	Rattus no
C 665	32	12.7	195637	2	AP002420	Homo sapi	C 738	32	12.7	235877	2	AC117278	AC117278	Rattus no
C 666	32	12.7	196083	2	AC027092	Homo sapi	739	32	12.7	235918	2	AC127741	AC127741	Rattus no
C 667	32	12.7	196119	2	AP001799	Homo sapi	C 740	32	12.7	235933	2	AC097843	AC097843	Rattus no
C 668	32	12.7	196146	2	AC023609	Mus muscu	C 741	32	12.7	236303	2	AC102981	AC102981	Rattus no
C 669	32	12.7	196990	2	AC134013	Rattus no	C 742	32	12.7	236402	2	AC120673	AC120673	Rattus no
C 670	32	12.7	198248	2	AP001487	Homo sapi	C 743	32	12.7	236527	2	AC134501	AC134501	Rattus no
C 671	32	12.7	198782	2	AC144252	Macaca mu	744	32	12.7	236550	2	AC111801	AC111801	Rattus no
C 672	32	12.7	199263	2	BX004992	Danio rer	C 745	32	12.7	236957	2	AC118153	AC118153	Rattus no
C 673	32	12.7	199301	2	BX088589	Danio rer	C 746	32	12.7	237192	2	AC013375	AC013375	Homo sapi
C 674	32	12.7	199733	2	AC107482	Mus muscu	747	32	12.7	237838	2	AC121282	AC121282	Mus muscu
C 675	32	12.7	200000	2	AC008076	Homo sapi	748	32	12.7	238285	2	AC109573	AC109573	Rattus no
C 676	32	12.7	201094	2	AC020995	Homo sapi	749	32	12.7	238839	2	AC123162	AC123162	Rattus no
C 677	32	12.7	201929	2	AC126087	Rattus no	C 750	32	12.7	239398	2	AC105708	AC105708	Rattus no
C 678	32	12.7	202033	2	BX511251	Danio rer	C 751	32	12.7	239851	2	AC101712	AC101712	Mus muscu
C 679	32	12.7	202878	2	AC137548	Macaca mu	752	32	12.7	239880	2	AC095415	AC095415	Rattus no
C 680	32	12.7	204990	2	AC138163	Bos tauru	753	32	12.7	239915	2	AC097168	AC097168	Rattus no
C 681	32	12.7	205158	2	AC015703	Homo sapi	C 754	32	12.7	239986	2	AC097238	AC097238	Rattus no
C 682	32	12.7	206159	2	AC107737	Mus muscu	755	32	12.7	240561	2	AC108554	AC108554	Rattus no
C 683	32	12.7	207193	2	AC137471	Rattus no	756	32	12.7	241109	2	AC106232	AC106232	Rattus no
C 684	32	12.7	207588	2	AC087162	Mus muscu	757	32	12.7	241587	2	AC096197	AC096197	Rattus no
C 685	32	12.7	208180	2	AC116722	Mus muscu	C 758	32	12.7	241725	2	AC112295	AC112295	Rattus no
C 686	32	12.7	208936	2	AC141215	Rattus no	C 759	32	12.7	241865	2	AC118396	AC118396	Rattus no
C 687	32	12.7	210752	2	AC098606	Rattus no	C 760	32	12.7	242882	2	AC094356	AC094356	Rattus no
C 688	32	12.7	211341	2	AC103309	Rattus no	C 761	32	12.7	243739	2	AC095239	AC095239	Rattus no
C 689	32	12.7	211375	2	AC141149	Rattus no	C 762	32	12.7	243789	2	AC136416	AC136416	Rattus no
C 690	32	12.7	211973	2	AP001163	Homo sapi	C 763	32	12.7	243884	2	AC130044	AC130044	Rattus no
C 691	32	12.7	213514	2	AC079500	Mus muscu	C 764	32	12.7	244389	2	AC111858	AC111858	Rattus no
C 692	32	12.7	213947	2	AC135988	Homo sapi	C 765	32	12.7	245394	2	AC125756	AC125756	Rattus no
C 693	32	12.7	214767	2	AC103390	Mus muscu	C 766	32	12.7	245832	2	AC107095	AC107095	Rattus no
C 694	32	12.7	215495	2	AC121649	Rattus no	C 767	32	12.7	246337	2	AC106484	AC106484	Rattus no
C 695	32	12.7	215541	2	AC016904	Homo sapi	C 768	32	12.7	246387	2	AC109737	AC109737	Rattus no
C 696	32	12.7	217028	2	AC140694	Rattus no	C 769	32	12.7	246710	2	AC094240	AC094240	Rattus no
C 697	32	12.7	217236	2	AC131344	Rattus no	C 770	32	12.7	247017	2	AC105601	AC105601	Rattus no
C 698	32	12.7	217822	2	AC131135	Rattus no	C 771	32	12.7	247659	2	AC095548	AC095548	Rattus no
C 699	32	12.7	219752	2	AC115297	Mus muscu	C 772	32	12.7	248449	2	AC137398	AC137398	Rattus no
C 700	32	12.7	219949	2	AC105796	Rattus no	C 773	32	12.7	248664	2	AC133854	AC133854	Rattus no
C 701	32	12.7	221260	2	AC122444	Mus muscu	774	32	12.7	248682	2	AC095449	AC095449	Rattus no
C 702	32	12.7	221962	2	AC136580	Rattus no	C 775	32	12.7	248720	2	AC114351	AC114351	Rattus no
C 703	32	12.7	222072	2	AC141069	Homo sapi	C 776	32	12.7	249131	2	AC121717	AC121717	Rattus no
C 704	32	12.7	223090	2	AC111554	Rattus no	777	32	12.7	250683	2	AC115272	AC115272	Rattus no
C 705	32	12.7	223225	2	AC112468	Rattus no	C 778	32	12.7	251703	2	AC114450	AC114450	Rattus no
C 706	32	12.7	223687	2	AC121373	Rattus no	C 779	32	12.7	252215	2	AC137271	AC137271	Rattus no
C 707	32	12.7	223875	2	AC133941	Mus muscu	C 780	32	12.7	252715	2	AC127819	AC127819	Rattus no
C 708	32	12.7	224031	2	AC137234	Rattus no	781	32	12.7	252925	2	AC021048	AC021048	Homo sapi
C 709	32	12.7	224726	2	AC097428	Rattus no	782	32	12.7	253067	2	AC142237	AC142237	Rattus no
C 710	32	12.7	224758	2	AC128387	Rattus no	C 783	32	12.7	253752	2	AC109934	AC109934	Rattus no
C 711	32	12.7	225154	2	AC106152	Rattus no	C 784	32	12.7	254217	2	AC114075	AC114075	Rattus no
C 712	32	12.7	225973	2	AC114232	Rattus no	C 785	32	12.7	254668	2	AC109742	AC109742	Rattus no
C 713	32	12.7	226077	2	AC013296	Homo sapi	C 786	32	12.7	254721	2	AC120733	AC120733	Rattus no
C 714	32	12.7	226135	2	AC110712	Rattus no	787	32	12.7	255032	2	AC107178	AC107178	Rattus no
C 715	32	12.7	227224	2	AC094832	Rattus no	C 788	32	12.7	255641	2	AC096524	AC096524	Rattus no
C 716	32	12.7	227767	2	AC118766	Rattus no	C 789	32	12.7	255713	2	AC099293	AC099293	Rattus no
C 717	32	12.7	227827	2	AC131809	Rattus no	C 790	32	12.7	256290	2	AC098754	AC098754	Rattus no
C 718	32	12.7	228052	2	AC094440	Rattus no	C 791	32	12.7	256348	2	AC095686	AC095686	Rattus no
C 719	32	12.7	228653	2	AC098441	Rattus no	792	32	12.7	256433	2	AC101703	AC101703	Mus muscu
C 720	32	12.7	229506	2	AL161933	Homo sapi	C 793	32	12.7	256643	2	AC122567	AC122567	Rattus no
C 721	32	12.7	229701	2	AC140109	Mus muscu	C 794	32	12.7	257444	2	AC099424	AC099424	Rattus no
C 722	32	12.7	229849	2	AC128399	Rattus no	C 795	32	12.7	257677	2	AC095819	AC095819	Rattus no

C 796	32	12.7	257679	2	AC134801	AC134801 Rattus no	869	31	12.4	20674	2	AC136474	AC136474 Homo sapi
C 797	32	12.7	258303	2	AC095938	AC095938 Rattus no	C 870	31	12.4	20712	2	AC013425	AC013425 Drosophila
C 798	32	12.7	258593	2	AC108965	AC108965 Rattus no	C 871	31	12.4	23788	2	AC068201	AC068201 Homo sapi
C 799	32	12.7	259631	2	AC095168	AC095168 Rattus no	C 872	31	12.4	27709	2	LMFLCHR32_27	Continuation (28 o
C 800	32	12.7	259694	2	AC139848	AC139848 Mus muscu	C 873	31	12.4	29590	2	AC015588	AC015588 Homo sapi
C 801	32	12.7	260017	2	AC098371	AC098371 Rattus no	C 874	31	12.4	29590	2	AC015588	AC015588 Homo sapi
C 802	32	12.7	260024	2	AC095715	AC095715 Rattus no	C 875	31	12.4	30237	2	AC115096	AC115096 Homo sapi
C 803	32	12.7	260573	2	AC125775	AC125775 Rattus no	C 876	31	12.4	30758	2	CEH08104	Z94122 Caenorhabdi
C 804	32	12.7	260805	2	AC097233	AC097233 Rattus no	C 877	31	12.4	34241	2	CEH25F02	Z93633 Caenorhabdi
C 805	32	12.7	261061	2	AC127435	AC127435 Rattus no	C 878	31	12.4	34145	2	AC079312	AC079312 Homo sapi
C 806	32	12.7	261604	2	AC119819	AC119819 Mus muscu	C 879	31	12.4	34886	2	AC133621	AC133621 Rattus no
C 807	32	12.7	261825	2	AC106351	AC106351 Rattus no	C 880	31	12.4	35195	2	AC068589	AC068589 Homo sapi
C 808	32	12.7	262061	2	AC117172	AC117172 Rattus no	C 881	31	12.4	35102	2	AC101082	AC101082 Mus muscu
C 809	32	12.7	262386	2	AC126101	AC126101 Rattus no	C 882	31	12.4	35546	2	AC100555	AC100555 Mus muscu
C 810	32	12.7	262984	2	AC095212	AC095212 Rattus no	C 883	31	12.4	37887	2	AC068453	AC068453 Homo sapi
C 811	32	12.7	265985	2	AC087226	AC087226 Mus muscu	C 884	31	12.4	38271	2	AC100969	AC100969 Mus muscu
C 812	32	12.7	267188	2	AC135827	AC135827 Rattus no	C 885	31	12.4	38824	2	AC087716	AC087716 Homo sapi
C 813	32	12.7	268279	2	AC097205	AC097205 Rattus no	C 886	31	12.4	39049	2	AC137692	AC137692 Mus muscu
C 814	32	12.7	272675	2	AC114467	AC114467 Rattus no	C 887	31	12.4	39186	2	AC136757	AC136757 Homo sapi
C 815	32	12.7	275351	2	AC117883	AC117883 Rattus no	C 888	31	12.4	40125	2	AC132818	AC132818 Homo sapi
C 816	32	12.7	276168	2	AC105518	AC105518 Rattus no	C 889	31	12.4	40764	2	AC126382	AC126382 Homo sapi
C 817	32	12.7	279112	2	AC132048	AC132048 Rattus no	C 890	31	12.4	41132	2	AC022741	AC022741 Homo sapi
C 818	32	12.7	279233	2	AC132167	AC132167 Rattus no	C 891	31	12.4	41356	2	AC069190	AC069190 Homo sapi
C 819	32	12.7	279587	2	AC112408	AC112408 Rattus no	C 892	31	12.4	41398	2	AC104853	AC104853 Homo sapi
C 820	32	12.7	284442	2	AC107002	AC107002 Rattus no	C 893	31	12.4	41399	2	AC129587	AC129587 Mus muscu
C 821	32	12.7	284442	2	AC096696	AC096696 Rattus no	C 894	31	12.4	42029	2	AC114762	AC114762 Homo sapi
C 822	32	12.7	280179	2	AC134072	AC134072 Rattus no	C 895	31	12.4	42170	2	AC104252	AC104252 Homo sapi
C 823	32	12.7	290633	2	AC099180	AC099180 Rattus no	C 896	31	12.4	42293	2	AC023531	AC023531 Homo sapi
C 824	32	12.7	291205	2	AC103125	AC103125 Rattus no	C 897	31	12.4	42614	2	AC127805_4	Continuation (5 of
C 825	32	12.7	293507	2	AC097292	AC097292 Rattus no	C 898	31	12.4	42818	2	AC13249	AC13249 Homo sapi
C 826	32	12.7	295708	2	AC102357	AC102357 Mus muscu	C 899	31	12.4	43295	2	AC024381	AC024381 Homo sapi
C 827	32	12.7	298503	2	AC102645	AC102645 Mus muscu	C 900	31	12.4	44005	2	AC104755	AC104755 Homo sapi
C 828	32	12.7	298532	2	AC129468	AC129468 Rattus no	C 901	31	12.4	44069	2	AC133288	AC133288 Homo sapi
C 829	32	12.7	305911	2	AC115447	AC115447 Rattus no	C 902	31	12.4	46397	2	AC134159	AC134159 Rattus no
C 830	32	12.7	306103	2	AC127202	AC127202 Rattus no	C 903	31	12.4	46405	2	AC027255	AC027255 Homo sapi
C 831	32	12.7	309771	2	AC117311	AC117311 Rattus no	C 904	31	12.4	46595	2	AC101015	AC101015 Mus muscu
C 832	32	12.7	314959	2	AC106099	AC106099 Rattus no	C 905	31	12.4	46742	2	AC100281	AC100281 Mus muscu
C 833	32	12.7	318620	2	AC110910	AC110910 Mus muscu	C 906	31	12.4	46889	2	AC091081	AC091081 Homo sapi
C 834	32	12.7	321777	2	AC118532	AC118532 Rattus no	C 907	31	12.4	47269	2	AC068834	AC068834 Homo sapi
C 835	32	12.7	322361	2	AC139220	AC139220 Mus muscu	C 908	31	12.4	47417	2	AC100702	AC100702 Mus muscu
C 836	32	12.7	326209	2	AC134065	AC134065 Rattus no	C 909	31	12.4	47425	2	AC009934	AC009934 Homo sapi
C 837	32	12.7	326739	2	AC142901	AC142901 Macaca mu	C 910	31	12.4	47533	2	AC101284	AC101284 Mus muscu
C 838	32	12.7	331675	2	AC097919	AC097919 Rattus no	C 911	31	12.4	47768	2	AC109310	AC109310 Homo sapi
C 839	32	12.7	337720	2	AC121050	AC121050 Rattus no	C 912	31	12.4	48460	2	AC101029	AC101029 Mus muscu
C 840	32	12.7	338453	2	AC112044	AC112044 Rattus no	C 913	31	12.4	48506	2	AC025671	AC025671 Homo sapi
C 841	32	12.7	342586	2	AC109682	AC109682 Rattus no	C 914	31	12.4	49397	2	AC087640	AC087640 Homo sapi
C 842	32	12.7	343504	2	AC158031	AC158031 Homo sapi	C 915	31	12.4	49580	2	AC136347	AC136347 Homo sapi
C 843	31	12.4	121	11	G42786	G42786 B5M66 Plaem	C 916	31	12.4	49976	2	AC025670	AC025670 Homo sapi
C 844	31	12.4	409	6	AX677607	AX677607 Sequence	C 917	31	12.4	50139	2	AC068883	AC068883 Homo sapi
C 845	31	12.4	513	3	AV175837	AV175837 Laupala k	C 918	31	12.4	50215	2	AC060819	AC060819 Homo sapi
C 846	31	12.4	513	3	AV175840	AV175840 Laupala h	C 919	31	12.4	50215	2	AC060819	AC060819 Homo sapi
C 847	31	12.4	736	8	AY216600	AY216600 Juncus pa	C 920	31	12.4	50411	2	AC087304	AC087304 Homo sapi
C 848	31	12.4	1075	6	AR231970	AR231970 Sequence	C 921	31	12.4	50487	2	AC068211	AC068211 Homo sapi
C 849	31	12.4	1075	6	BD135520	BD135520 Neurotrop	C 922	31	12.4	50905	2	AC099853	AC099853 Mus muscu
C 850	31	12.4	1076	6	AR231986	AR231986 Sequence	C 923	31	12.4	51234	2	AC102920	AC102920 Mus muscu
C 851	31	12.4	1214	8	PSWRR18S	LI6011 Pseudowinte	C 924	31	12.4	51275	2	AC090351	AC090351 Homo sapi
C 852	31	12.4	1402	8	AF146215	AF146215 Marzaella	C 925	31	12.4	51340	2	AC025213	AC025213 Homo sapi
C 853	31	12.4	1428	8	AX297639	Z97639 Acantholimo	C 926	31	12.4	51381	2	AC136770	AC136770 Homo sapi
C 854	31	12.4	1462	8	AF284902	AF284902 Carex dig	C 927	31	12.4	51754	2	AC129479	AC129479 Mus muscu
C 855	31	12.4	1471	8	AF284899	AF284899 Carex lim	C 928	31	12.4	51883	2	AC135993	AC135993 Homo sapi
C 856	31	12.4	1494	8	AF284907	AF284907 Carex lan	C 929	31	12.4	52302	2	AC099867	AC099867 Mus muscu
C 857	31	12.4	1560	6	AX513749	AX513749 Sequence	C 930	31	12.4	52614	2	AC090899	AC090899 Mus muscu
C 858	31	12.4	1666	8	AF284916	AF284916 Carex mac	C 931	31	12.4	52783	2	AC100403	AC100403 Mus muscu
C 859	31	12.4	1675	8	AF284900	AF284900 Carex ova	C 932	31	12.4	52806	2	AC090158	AC090158 Homo sapi
C 860	31	12.4	2157	6	AR231967	AR231967 Sequence	C 933	31	12.4	53121	2	AC136331	AC136331 Homo sapi
C 861	31	12.4	2157	6	BD135517	BD135517 Neurotrop	C 934	31	12.4	53435	2	AC135259	AC135259 Homo sapi
C 862	31	12.4	2158	6	AR231983	AR231983 Sequence	C 935	31	12.4	53439	2	AC140621	AC140621 Macaca mu
C 863	31	12.4	2568	6	AR231959	AR231959 Sequence	C 936	31	12.4	53581	2	AC120351	AC120351 Mus muscu
C 864	31	12.4	2568	6	BD135509	BD135509 Neurotrop	C 937	31	12.4	53659	2	AC013255	AC013255 Drosophila
C 865	31	12.4	3209	6	AR231961	AR231961 Sequence	C 938	31	12.4	53871	2	AC132821	AC132821 Homo sapi
C 866	31	12.4	3209	6	AR231977	AR231977 Sequence	C 939	31	12.4	54245	2	AC100907	AC100907 Mus muscu
C 867	31	12.4	3209	6	BD135511	BD135511 Neurotrop	C 940	31	12.4	54257	2	AC100202	AC100202 Mus muscu
C 868	31	12.4	15503	2	AC125536	AC125536 Mus muscu	C 941	31	12.4	54383	2	AC100305	AC100305 Mus muscu

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c 942 31 12.4 54450 2 AC080179 Homo sapi
c 943 31 12.4 54452 2 AC103860 Homo sapi
c 944 31 12.4 54612 2 AC103821 Homo sapi
c 945 31 12.4 54706 2 AC100048 Mus muscu
c 946 31 12.4 54777 2 AC013651 Homo sapi
c 947 31 12.4 54958 2 AC090760 Homo sapi
c 948 31 12.4 55238 2 AC013422 Drosophi
c 949 31 12.4 55283 2 AC100610 Mus muscu
c 950 31 12.4 55774 2 AC091303 Homo sapi
c 951 31 12.4 55801 2 AC087476 Homo sapi
c 952 31 12.4 55973 2 AC079107 Homo sapi
c 953 31 12.4 56083 2 AC141162 Rattus no
c 954 31 12.4 56133 2 AC115998 Homo sapi
c 955 31 12.4 56134 2 AC132199 Homo sapi
c 956 31 12.4 56328 2 AC068514 Homo sapi
c 957 31 12.4 56507 2 AC055770 Homo sapi
c 958 31 12.4 56970 2 AC138096 Homo sapi
c 959 31 12.4 57028 2 AC131078 Mus muscu
c 960 31 12.4 57058 2 AC069455 Homo sapi
c 961 31 12.4 57258 2 AC130342 Homo sapi
c 962 31 12.4 57448 2 AC013539 Homo sapi
c 963 31 12.4 57591 2 AC069490 Homo sapi
c 964 31 12.4 57671 2 AC124003 Homo sapi
c 965 31 12.4 57843 2 AC110290 Homo sapi
c 966 31 12.4 57843 2 AC136651 Rattus no
c 967 31 12.4 57877 2 AC100077 Mus muscu
c 968 31 12.4 58040 2 AC101628 Mus muscu
c 969 31 12.4 58081 2 AC010841 Drosophi
c 970 31 12.4 58090 2 AC105092 Homo sapi
c 971 31 12.4 58172 2 AC083793 Homo sapi
c 972 31 12.4 58207 2 AC136762 Homo sapi
c 973 31 12.4 58261 2 AC1394894 Continuation (5 of
c 974 31 12.4 58279 2 AC104354 Homo sapi
c 975 31 12.4 58329 2 AC118271 Homo sapi
c 976 31 12.4 58508 2 AC100320 Mus muscu
c 977 31 12.4 58560 2 AC131048 Homo sapi
c 978 31 12.4 58603 2 AC101496 Mus muscu
c 979 31 12.4 58666 2 AC090594 Homo sapi
c 980 31 12.4 59006 2 AC118054 Homo sapi
c 981 31 12.4 59061 2 AC090749 Homo sapi
c 982 31 12.4 59445 2 AC090596 Homo sapi
c 983 31 12.4 59731 2 AC067830 Homo sapi
c 984 31 12.4 59763 2 AC137116 Mus muscu
c 985 31 12.4 59770 2 AC084259 Homo sapi
c 986 31 12.4 59815 2 AC100984 Homo sapi
c 987 31 12.4 59926 2 AC107461 Homo sapi
c 988 31 12.4 59928 2 AC068229 Homo sapi
c 989 31 12.4 59967 2 AC073302 Homo sapi
c 990 31 12.4 60108 2 AC090854 Homo sapi
c 991 31 12.4 60190 2 AC127498 Homo sapi
c 992 31 12.4 60265 2 AC073445 Homo sapi
c 993 31 12.4 60329 2 AC091109 Homo sapi
c 994 31 12.4 60456 2 AC087634 Homo sapi
c 995 31 12.4 60504 2 AC090716 Homo sapi
c 996 31 12.4 60661 2 AC024389 Homo sapi
c 997 31 12.4 60814 2 AC073622 Homo sapi
c 998 31 12.4 60958 2 AC132203 Homo sapi
c 999 31 12.4 60995 2 AC0961193 Continuation (4 of
c1000 31 12.4 61010 2 AC087492 Homo sapi

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## ALIGNMENTS

```

RESULT 1
AC015736
LOCUS AC015736 77433 bp DNA linear HTG 13-JUL-2000
DEFINITION Homo sapiens clone RP11-1D13, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC015736
VERSION AC015736.2 GI:9108790
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 77433)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-1D13
Unpublished
2 (bases 1 to 77433)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Balwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Collangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Furke,R., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howard,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi.6448951.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: Li436
Center Clone name: 1_D_13
-----
* NOTE: This record contains 76 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 868: contig of 868 bp in length
* 869 968: gap of 100 bp
* 969 1903: contig of 935 bp in length
* 1904 2003: gap of 100 bp
* 2004 2884: contig of 881 bp in length
* 2885 3916: contig of 932 bp in length
* 3917 4016: gap of 100 bp
* 4017 4937: contig of 921 bp in length
* 4938 5037: gap of 100 bp
* 5038 5940: contig of 903 bp in length
* 5941 6040: gap of 100 bp
* 6041 6959: contig of 919 bp in length
* 6960 7059: gap of 100 bp
* 7060 7874: contig of 915 bp in length
* 7875 8074: gap of 100 bp
* 8075 9019: contig of 945 bp in length
* 9020 10046: contig of 927 bp in length
* 10047 10146: gap of 100 bp
* 10147 11053: contig of 907 bp in length
* 11054 11153: gap of 100 bp
* 11154 12059: contig of 906 bp in length
* 12060 12159: gap of 100 bp
* 12160 13077: contig of 918 bp in length

```

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## COMMENT



JOURNAL  
REFERENCE  
AUTHORS

Published Only in DataBase (2000)

2 (bases 1 to 211452)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.TITLE  
JOURNAL

Direct Submission

Submitted (08-MAY-2000) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

Kitasato Univ., 1-15-1 Kitasato, Sagami-hara, Kanagawa 228-8555,

Japan [E-mail: hattori@gsc.riken.go.jp,

URL: http://hgp.gsc.riken.go.jp/, Tel: 81-42-778-9923,

Fax: 81-42-778-9924)

On May 30, 2000 this sequence version replaced gi:7768935.

## COMMENT

----- Genome Center

Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: http://hgp.gsc.riken.go.jp/

Contact: hattori@gsc.riken.go.jp

----- Project Information

Center project name: HumDraft11

Center clone name: Rp11-880P3

----- Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator ET-amersham; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 189257 bases at least Q40

Consensus quality: 200319 bases at least Q30

Consensus quality: 205564 bases at least Q20

Insert size: 208152; sum-of-contigs

Quality coverage: 4.07x in Q20 bases; sum-of-contigs

-----

NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1 28021 contig of 28021 bp in length  
 28122 42064 contig of 13943 bp in length  
 54544 42165 54544 contig of 12380 bp in length  
 54645 68334 contig of 12290 bp in length  
 67035 78065 contig of 11031 bp in length  
 78166 85965 contig of 7800 bp in length  
 86066 94021 contig of 7956 bp in length  
 94122 103137 contig of 9016 bp in length  
 103238 110428 contig of 7191 bp in length  
 110529 117362 contig of 6774 bp in length  
 124236 130599 contig of 6364 bp in length  
 130700 136620 contig of 5921 bp in length  
 136721 143251 contig of 6531 bp in length  
 143352 149360 contig of 6009 bp in length  
 149361 149460 contig of 100 bp in length  
 149461 154813 contig of 5353 bp in length  
 154814 154914 contig of 100 bp in length  
 154914 160815 160914 contig of 5901 bp in length  
 160815 160915 160914 contig of 5901 bp in length  
 160915 165831 165930 contig of 4916 bp in length  
 165831 171277 contig of 5347 bp in length  
 171278 171377 contig of 100 bp in length  
 171378 175018 contig of 3641 bp in length  
 175019 175119 contig of 4064 bp in length  
 175119 179183 179282 contig of 4064 bp in length  
 179183 183958 contig of 4676 bp in length  
 183959 184059 184058 contig of 100 bp in length  
 184059 188202 contig of 4144 bp in length  
 188203 188303 188302 contig of 100 bp in length  
 188303 191129 contig of 2827 bp in length  
 191130 191229 contig of 100 bp in length  
 191230 194326 contig of 3097 bp in length  
 194327 194427 194426 contig of 100 bp in length  
 194427 197544 197543 contig of 3117 bp in length  
 197544 197644 197643 contig of 100 bp in length  
 197644 200559 contig of 2916 bp in length  
 200559 203056 contig of 100 bp in length  
 203057 203157 203156 contig of 2397 bp in length  
 203157 205136 contig of 1980 bp in length  
 205137 206801 contig of 1565 bp in length  
 206801 206902 206901 contig of 1565 bp in length  
 206902 207589 contig of 688 bp in length  
 207589 207690 207689 contig of 1459 bp in length  
 207690 209249 209248 contig of 1011 bp in length  
 209249 210360 210359 contig of 1093 bp in length  
 210360 211452 contig of 1093 bp in length

Sequence updated (26-May-2000).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 34 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 28021: contig of 28021 bp in length  
 28022 28121: gap of 100 bp  
 28122 42064: contig of 13943 bp in length  
 42065 42164: gap of 100 bp  
 42165 54544: contig of 12380 bp in length  
 54545 54644: gap of 100 bp  
 54645 68334: contig of 12290 bp in length  
 68335 78065: gap of 100 bp  
 78066 78165: gap of 100 bp  
 78166 85965: contig of 7800 bp in length  
 85966 94021: contig of 7956 bp in length  
 94022 94121: gap of 100 bp  
 94122 103137: contig of 9016 bp in length  
 103138 103237: gap of 100 bp  
 103238 110428: contig of 7191 bp in length  
 110429 110528: gap of 100 bp  
 110529 117261: contig of 6733 bp in length  
 117262 117361: gap of 100 bp  
 117362 124135: contig of 6774 bp in length  
 124136 124235: gap of 100 bp  
 124236 130599: contig of 6364 bp in length  
 130600 130699: gap of 100 bp  
 130700 136620: contig of 5921 bp in length  
 136621 136720: gap of 100 bp  
 136721 143251: contig of 6531 bp in length  
 143252 143351: gap of 100 bp  
 143352 149360: contig of 6009 bp in length  
 149361 149460: gap of 100 bp  
 149461 154813: contig of 5353 bp in length  
 154814 154913: gap of 100 bp  
 154914 160814: contig of 5901 bp in length  
 160815 160914: gap of 100 bp  
 160915 165830: contig of 4916 bp in length  
 165831 165930: gap of 100 bp  
 165931 171277: contig of 5347 bp in length  
 171278 171377: gap of 100 bp  
 171378 175018: contig of 3641 bp in length  
 175019 175118: gap of 100 bp  
 175119 179182: contig of 4064 bp in length  
 179183 179282: gap of 100 bp  
 179283 183958: contig of 4676 bp in length  
 183959 184058: gap of 100 bp  
 184059 188202: contig of 4144 bp in length  
 188203 188302: gap of 100 bp  
 188303 191129: contig of 2827 bp in length  
 191130 191229: gap of 100 bp  
 191230 194326: contig of 3097 bp in length  
 194327 194426: gap of 100 bp  
 194427 197543: contig of 3117 bp in length  
 197544 197643: gap of 100 bp  
 197644 200559: contig of 2916 bp in length  
 200559 203056: gap of 100 bp  
 203057 203156: gap of 100 bp  
 203157 205136: contig of 1980 bp in length  
 205137 205236: gap of 100 bp  
 205237 206801: contig of 1565 bp in length  
 206802 206901: gap of 100 bp  
 206902 207589: contig of 688 bp in length  
 207589 207689: gap of 100 bp  
 207690 209148: contig of 1459 bp in length  
 209149 209248: gap of 100 bp  
 209249 210259: contig of 1011 bp in length  
 210260 210359: gap of 100 bp









McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,  
 Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
 Murphy,T., Naylor,T., Norman,C.H., O'Connor,I., O'Donnell,P.,  
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
 Vassiliev,H., Vied,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

# TITLE JOURNAL

Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:

## COMMENT

Smit,A.F.A. & Green,P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L8146  
 Center clone name: 440\_H\_3  
 -----

\* NOTE: This record contains 86 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.

1 694: contig of 694 bp in length  
 695 794: gap of 100 bp  
 795 1531: contig of 737 bp in length  
 1532 1631: gap of 100 bp  
 1632 2364: contig of 733 bp in length  
 2365 2464: gap of 100 bp  
 2465 3205: contig of 741 bp in length  
 3206 3305: gap of 100 bp  
 3306 4012: contig of 707 bp in length  
 4013 4112: gap of 100 bp  
 4113 4818: contig of 706 bp in length  
 4819 4918: gap of 100 bp  
 4919 5609: contig of 691 bp in length  
 5610 5709: gap of 100 bp  
 5710 6413: contig of 704 bp in length  
 6414 6513: gap of 100 bp  
 6514 7217: contig of 704 bp in length  
 7218 7317: gap of 100 bp  
 7318 8038: contig of 721 bp in length  
 8039 8138: gap of 100 bp  
 8139 8844: contig of 706 bp in length  
 8845 8945: gap of 100 bp  
 8945 9653: contig of 709 bp in length  
 9654 9753: gap of 100 bp  
 9754 10471: contig of 718 bp in length  
 10472 11253: contig of 682 bp in length  
 11254 11353: gap of 100 bp  
 11354 12069: contig of 716 bp in length  
 12070 12169: gap of 100 bp  
 12170 12877: contig of 708 bp in length  
 12878 12977: gap of 100 bp  
 12978 13684: contig of 707 bp in length  
 13685 13784: gap of 100 bp  
 13785 14479: contig of 695 bp in length  
 14480 14579: gap of 100 bp  
 14580 15302: contig of 723 bp in length

15402: gap of 100 bp  
 16107: contig of 705 bp in length  
 16207: gap of 100 bp  
 16208 16930: contig of 723 bp in length  
 17031 17030: gap of 100 bp  
 17031 17766: contig of 736 bp in length  
 17767 17866: gap of 100 bp  
 17867 18590: contig of 724 bp in length  
 18591 18690: gap of 100 bp  
 18691 19399: contig of 709 bp in length  
 19400 19499: gap of 100 bp  
 20201: contig of 702 bp in length  
 20302 20301: gap of 100 bp  
 21002: contig of 701 bp in length  
 21102: gap of 100 bp  
 21817: contig of 715 bp in length  
 21917: gap of 100 bp  
 22597: contig of 680 bp in length  
 22697: gap of 100 bp  
 23383: contig of 686 bp in length  
 23384 23483: gap of 100 bp  
 23484 24180: contig of 697 bp in length  
 24181 24280: gap of 100 bp  
 24281 24993: contig of 713 bp in length  
 24994 25093: gap of 100 bp  
 25094 25809: contig of 716 bp in length  
 25810 25909: gap of 100 bp  
 25910 26637: contig of 728 bp in length  
 26638 26737: gap of 100 bp  
 26738 27446: contig of 709 bp in length  
 27447 27546: gap of 100 bp  
 27547 28244: contig of 718 bp in length  
 28245 28364: gap of 100 bp  
 28365 29079: contig of 715 bp in length  
 29080 29179: gap of 100 bp  
 29180 29913: contig of 734 bp in length  
 29914 30013: gap of 100 bp  
 30014 30729: contig of 716 bp in length  
 30730 30829: gap of 100 bp  
 30830 31524: contig of 695 bp in length  
 31525 31624: gap of 100 bp  
 31625 32335: contig of 711 bp in length  
 32336 32435: gap of 100 bp  
 32436 33140: contig of 705 bp in length  
 33141 33240: gap of 100 bp  
 33241 33946: contig of 706 bp in length  
 33947 34046: gap of 100 bp  
 34047 34755: contig of 709 bp in length  
 34756 34855: gap of 100 bp  
 34856 35561: contig of 706 bp in length  
 35562 35661: gap of 100 bp  
 35662 36376: contig of 715 bp in length  
 36377 36476: gap of 100 bp  
 36477 37199: contig of 723 bp in length  
 37200 37299: gap of 100 bp  
 37300 38018: contig of 719 bp in length  
 38019 38118: gap of 100 bp  
 38119 38828: contig of 710 bp in length  
 38829 39636: contig of 708 bp in length  
 39637 39736: gap of 100 bp  
 39737 40449: contig of 713 bp in length  
 40450 40549: gap of 100 bp  
 40550 41255: contig of 706 bp in length  
 41256 41355: gap of 100 bp  
 41356 42068: contig of 713 bp in length  
 42069 42168: gap of 100 bp  
 42169 42873: contig of 705 bp in length  
 42874 42973: gap of 100 bp  
 42974 43694: contig of 721 bp in length  
 43695 44510: contig of 716 bp in length  
 44511 44610: gap of 100 bp



18021	18736: contig of 716 bp in length
18737	18836: gap of 100 bp
18837	19563: contig of 727 bp in length
19564	19663: gap of 100 bp
19664	20411: contig of 748 bp in length
20412	20511: gap of 100 bp
20512	21253: contig of 742 bp in length
21254	21353: gap of 100 bp
21354	22070: contig of 717 bp in length
22071	22170: gap of 100 bp
22171	22874: contig of 704 bp in length
22875	22974: gap of 100 bp
22976	23686: contig of 712 bp in length
23687	23786: gap of 100 bp
23787	24499: contig of 713 bp in length
24499	24599: gap of 100 bp
24500	25290: contig of 691 bp in length
25291	25390: gap of 100 bp
25391	26114: contig of 724 bp in length
26115	26214: gap of 100 bp
26215	26932: contig of 718 bp in length
26932	27032: gap of 100 bp
27033	27761: contig of 729 bp in length
27762	27861: gap of 100 bp
27862	28568: contig of 707 bp in length
28569	28668: gap of 100 bp
28669	29336: contig of 728 bp in length
29337	29496: gap of 100 bp
29497	30228: contig of 732 bp in length
30229	30328: gap of 100 bp
30329	31045: contig of 717 bp in length
31046	31145: gap of 100 bp
31146	31845: contig of 700 bp in length
31846	31945: gap of 100 bp
31946	32628: contig of 683 bp in length
32629	32728: gap of 100 bp
32729	33454: contig of 726 bp in length
33455	33554: gap of 100 bp
33555	34265: contig of 711 bp in length
34266	34365: gap of 100 bp
34366	35063: contig of 698 bp in length
35066	35163: gap of 100 bp
35164	35863: contig of 700 bp in length
35864	35963: gap of 100 bp
35964	36682: contig of 719 bp in length
36683	36782: gap of 100 bp
36783	37489: contig of 707 bp in length
37490	37589: gap of 100 bp
37590	38325: contig of 736 bp in length
38326	38425: gap of 100 bp
38426	39178: contig of 753 bp in length
39179	39278: gap of 100 bp
39279	39979: contig of 721 bp in length
40000	40099: gap of 100 bp
40100	40804: contig of 705 bp in length
40805	40904: gap of 100 bp
40905	41594: contig of 690 bp in length
41595	41694: gap of 100 bp
41695	42405: contig of 711 bp in length
42406	42505: gap of 100 bp
42506	43224: contig of 719 bp in length
43225	43324: gap of 100 bp
43325	44033: contig of 709 bp in length
44034	44133: gap of 100 bp
44134	44834: contig of 701 bp in length
44835	44934: gap of 100 bp
44935	45670: contig of 736 bp in length
45671	45770: gap of 100 bp
45771	46500: contig of 730 bp in length
46501	46600: gap of 100 bp
46601	47331: contig of 731 bp in length
47332	47431: gap of 100 bp
47433	48172: contig of 741 bp in length

[illegible]

Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,U., Kovar,C.,  
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C.,  
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,  
Loulsegad,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,  
Ma,J., Maheshwari,M., Mapua,P., Marondel,I., Martin,R.,  
Martindale,A., Martinez,E., Massey,E., Mathew,B., McLeod,M.P.,  
Meador,M., Mei,G., Merscher,S., Metzker,M., Miller,A., Miner,G.,  
Miner,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M.,  
Morris,S., Mosser,M., Neal,D., Nelson,D., Newton,J., Newton,N.,  
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,  
Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,  
Peery,J., Perez,L., Peters,D., Pickens,R., Primus,E., Pu,L.L.,  
Quiles,M., Ren,Y., Rivers,A., Rojase,A., Rojibokan,I., Rolfe,M.,  
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shim,C.,  
Shooshitari,N., Sison,I., Sodergren,B., Sonaik,T., Sparks,A.,  
Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A.,  
Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B.,  
Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D.,  
Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R.,  
Washington,C., Watlington,S., Williams,G., Williamson,A.,  
Wleciyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J.,  
Zorrilla,S., Kucherlapati,R., Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

3 (bases 1 to 136479)

Direct Submission

Submitted (09-APR-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center -----

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information -----

Center project name: LCGE

Center clone name: CH250-271N4

----- Summary Statistics -----

Chemistry: Dye-primer Bodypy: inf% of reads

Chemistry: Dye-terminator Big Dye: inf% of reads

Consensus quality: 2515 bases at least Q40

Consensus quality: 3056 bases at least Q30

Consensus quality: 3728 bases at least Q20

-----

- \* NOTE: Estimated insert size may differ from sequence length
- \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))
- \* NOTE: The contigs are based on the application
- \* of the PGI method using the Human genome (NCBI build 31)
- \* as the comparative genome.
- \* NOTE: This is a 'working draft' sequence. It currently
- \* consists of 1 contigs. Gaps between the contigs
- \* are represented as runs of N. The order of the pieces
- \* is believed to be correct as runs of N. However the sizes
- \* of the gaps between them are based on estimates that have
- \* provided by the submitter.
- \* This sequence will be replaced
- \* by the finished sequence as soon as it is available and
- \* the accession number will be preserved.
- \* 1 136479: contig of 136479 bp in length.

Location/Qualifiers

1. 136479

/organism="Macaca mulatta"

/mol\_type="genomic DNA"

/db\_xref="taxon:9544"

/clone="CH250-271N4"

1. 136479

/note="assembly name:CH250-271N4.1B

CONFIDENCE: 0.83"

misc\_feature

1549 a 950 C 845 g 1576 t 131559 others

BASE COUNT

ORIGIN

Query Match

```

Best Local Similarity    100.0%;   Pred. NO. 3e-09;      Matches       35; Conservative     0; Mismatches         0; Indels           0; Gaps             0;

QY          100 NNNNNNNNNNNNNNNNNNNNNNNNTTCCAAAACC 134
            |||
DB          842 NNNNNNNNNNNNNNNNNNNNNNNNTTCCAAAACC 808
            |||


RESULT 8
AP005013/c
LOCUS
DEFINITION Homo sapiens chromosome 11 clone RP11-167H1 map llq, WORKING DRAFT SEQUENCE, 37 unordered pieces.
ACCESSION AP005013
VERSION   AP005013.1 GI:19773553
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Plrnatia; Catarrhini; Hominidae; Homo.
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     Homo sapiens genomic DNA of 11q.
JOURNAL   Published Only in Database (2002)
REFERENCE 2 (bases 1 to 140055)
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     Direct Submission
JOURNAL   Submitted (26-MAR-2002) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel.:81-45-503-9111, Fax:81-45-503-9170)
COMMENT   ----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-167H1
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amershaw; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 127324 bases at least Q40
Consensus quality: 133408 bases at least Q30
Consensus quality: 135610 bases at least Q20
Insert size: 136455; sum-of-contigs
Quality coverage: 4.20x in Q20 bases; sum-of-contigs
-----
NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved 1
              9720 contig of 9720 bp in length
                9821        18014 contig of 8194 bp in length
                 18115      26230 contig of 8116 bp in length
                  26331      34156 contig of 7826 bp in length
                   34257      40713 contig of 6457 bp in length
                    40814      47268 contig of 6455 bp in length
                     47369      54855 contig of 7487 bp in length
                      54956      60765 contig of 5910 bp in length
                       60866      65706 contig of 4740 bp in length
                        65706      70474 contig of 4769 bp in length
                         70575      74912 contig of 4338 bp in length
                          75013      80353 contig of 5341 bp in length
                           80454      84679 contig of 4226 bp in length
                            84780      88991 contig of 4212 bp in length

```



```

RESULT 9
LOCUS AC093306 158231 bp DNA linear HTG 16-AUG-2001
DEFINITION Homo sapiens chromosome 5 clone RP11-71K19, WORKING DRAFT SEQUENCE,
4 unordered pieces.
ACCESSION AC093306
VERSION AC093306.1 GI:15193440
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158231)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
2 (bases 1 to 158231)
DOE Joint Genome Institute.
Direct Submission
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 433888
Center clone name: RPC-11_71K19
-----
Summary Statistics
Consensus quality: 155197 bases at least Q40
Consensus quality: 156495 bases at least Q30
Consensus quality: 157279 bases at least Q20
Estimated insert size: 167260; agarose-fp estimation
Quality coverage: 11.02 in Q20 bases; sum-of-contigs estimation
Quality coverage: 11.67 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1000: contig of 1000 bp in length
* 1001 1100: gap of unknown length
* 1101 2270: contig of 1170 bp in length
* 2271 2370: gap of unknown length
* 2371 14042: contig of 11672 bp in length
* 14043 14142: gap of unknown length
* 14143 158231: contig of 144089 bp in length.
Location/Qualifiers
1..158231
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-71K19"
/clone.lib="RPC1 human BAC library 11"
BASE COUNT 47582 a 29021 c 28686 g 52623 t 319 others
ORIGIN
Query Match 13.9%; Score 35; DB 2; Length 158231;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

20 ACACAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
| | | | | | | | | | | | | | | | | | | | | |
db 991 ACACAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1025
| | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 10
LOCUS AC124963 160191 bp DNA linear HTG 14-MAY-2003
DEFINITION Medicago truncatula clone mth2-24f5, WORKING DRAFT SEQUENCE, 6
ordered pieces.
ACCESSION AC124963
VERSION AC124963.12 GI:30698573
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 160191)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-24f5
Unpublished
2 (bases 1 to 160191)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (20-JUN-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 160191)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (14-MAY-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On May 14, 2003 this sequence version replaced gi:30387683.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UONOR
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 13168: contig of 13168 bp in length
* 13169 13268: gap of unknown length
* 13269 29072: contig of 15804 bp in length
* 29073 29172: gap of unknown length
* 29173 50317: contig of 21145 bp in length
* 50318 50417: gap of unknown length
* 50418 74728: contig of 24311 bp in length
* 74729 74828: gap of unknown length
* 74829 115700: contig of 40872 bp in length
* 115701 115800: gap of unknown length
* 115801 160191: contig of 44391 bp in length.
Location/Qualifiers
1..160191
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/db_xref="taxon:3880"
/clone="mth2-24f5"
/clone.lib="Medicago truncatula BAC library H2"
BASE COUNT 53000 a 26397 c 26913 g 53374 t 507 others
ORIGIN
Query Match 13.9%; Score 35; DB 2; Length 160191;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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4876. .6066
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/note="assembly_name:Contig49"
7584. .9425
/note="assembly_name:Contig50"
9526. .10622
/note="assembly_name:Contig52"
10723. .11812
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11913. .13073
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13174. .14552
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15851. .17134
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17235. .18410
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18511. .19715
/note="assembly_name:Contig62"
19816. .21591
/note="assembly_name:Contig67"
21692. .22720
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/note="assembly_name:Contig75"
32618. .33728
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33829. .35653
/note="assembly_name:Contig77"
35754. .39536
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39637. .42666
/note="assembly_name:Contig79"
42767. .47200
/note="assembly_name:Contig80"
47301. .51035
/note="assembly_name:Contig81"
51136. .53256
/note="assembly_name:Contig82"
53357. .57404
/note="assembly_name:Contig83"
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Query Match 13.9%; Score 35; DB 2; Length 178521;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
90 ACACAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
|||||
18520 ACACAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 18486
```

RESULT 12

```
AP001484/c
LOCUS
DEFINITION
  Homo sapiens chromosome 18 clone RP11-635D8 map 18q21, WORKING
  DRAFT SEQUENCE, 41 unordered pieces.
ACCESSION
  AP001484
VERSION
  AP001484.2 GI:8117342
KEYWORDS
  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
  Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 185479)
    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
    Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  Homo sapiens 185,479 genomic DNA of 18q21
  2 (bases 1 to 185479)
    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
    Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  Direct Submission
  Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical
  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
  Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
  Japan (E-mail:hattori@gsc.riken.go.jp,
  URL:http://hgp-gsc.riken.go.jp/, Tel:81-42-778-9923,
  Fax:81-42-778-9924)
  On May 30, 2000 this sequence version replaced gi:7288178.
  ----- Genome Center
  Center: RIKEN Genomic Sciences Center (GSC)
  Center code: RIKEN
  Web site: http://hgp.gsc.riken.go.jp/
  Contact: hattori@gsc.riken.go.jp
  ----- Project Information
  Center project name: HumDrafc18
  Center clone name: RP11-635D8
  ----- Summary Statistics
  Sequencing vector: PCR products; 100% of reads
  Chemistry: Dye-terminator ET-amersham; 100% of reads
  Assembly program: Phrap; version 0.990329
  Consensus quality: 167208 bases at least Q40
  Consensus quality: 172243 bases at least Q30
  Consensus quality: 176665 bases at least Q20
  Insert size: 181479; sum-of-contigs
  Quality coverage: 5.04x in Q20 bases; sum-of-contigs
  -----
  NOTE: This is a 'working draft' sequence. It currently consists of
  41 contigs. The true order of the pieces is not known and their
  order in this sequence record is arbitrary. Gaps between the
  contigs are represented as runs N, but the exact sizes of the gaps
  are unknown. This record will be updated with the finished sequence
  as soon as it is available and the accession number will be
  preserved
  1 16288 contig of 16288 bp in length
  16389 25442 contig of 9054 bp in length
  25543 35229 contig of 9687 bp in length
  35330 43767 contig of 8438 bp in length
  43868 52274 contig of 8407 bp in length
  52375 60076 contig of 7702 bp in length
  60177 67220 contig of 7044 bp in length
  67321 73733 contig of 6413 bp in length
  73834 79587 contig of 5754 bp in length
  79688 86110 contig of 6423 bp in length
  86211 91829 contig of 5619 bp in length
  91930 98330 contig of 6401 bp in length
  98431 102918 contig of 4488 bp in length
  103019 107979 contig of 4961 bp in length
  108080 113581 contig of 5502 bp in length
  113682 117572 contig of 3891 bp in length
  117673 122375 contig of 3891 bp in length
  122476 127400 contig of 4703 bp in length
  127501 130555 contig of 4925 bp in length
  130656 134486 contig of 3055 bp in length
  134587 137488 contig of 2902 bp in length
```



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SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 230154)
AUTHORS    Muzny,D.,Maric,M., Metzker,M.,Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
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            Chacko,J., Chavez,D., Chen,G., Chen,K., Chen,Y., Chen,Z., Chu,J.,
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            Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R.,
            Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
            Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
            Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
            Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
            Direct Submission
            Unpublished
            2 (bases 1 to 230154)
            Worley,K.C.
            Direct Submission
            Submitted (28-FEB-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 230154)
            Worley,K.C.
            Direct Submission
            Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            ----- Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: KDPX
Center Clone name: CH230-6318
----- Summary Statistics
Sequencing Vector: Plasmid:
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.950329
Consensus quality: 194409 bases at least Q40
Consensus quality: 200156 bases at least Q30
Consensus quality: 204242 bases at least Q20
Estimated insert size: 201860; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) .
* NOTE: This is a "working draft" sequence. It currently
* consists of 72 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1121: contig of 1121 bp in length
* 1122 1221: gap of unknown length
* 1222 2311: contig of 1090 bp in length
* 2312 2411: gap of unknown length
* 2412 3545: contig of 1134 bp in length
* 3546 3645: gap of unknown length
* 3646 4881: contig of 1236 bp in length
* 4882 4981: gap of unknown length
* 4982 6010: contig of 1029 bp in length
* 6011 6110: gap of unknown length
* 6111 7203: contig of 1093 bp in length
* 7204 8496: contig of 1193 bp in length
* 8497 8596: gap of unknown length
* 8597 10255: contig of 1659 bp in length
* 10256 10355: gap of unknown length
* 10356 18099: contig of 1454 bp in length
* 11810 11909: gap of unknown length
* 11910 13265: contig of 1356 bp in length
* 13266 13365: gap of unknown length
* 13366 15347: contig of 1982 bp in length
* 15348 15447: gap of unknown length
* 15448 16840: contig of 1393 bp in length
* 16841 16940: gap of unknown length
* 16941 18100: contig of 1160 bp in length
* 18101 18200: gap of unknown length
* 18201 19780: contig of 1580 bp in length
* 19781 19880: gap of unknown length
* 19881 21405: contig of 1525 bp in length
* 21406 21505: gap of unknown length
* 21506 22808: contig of 1303 bp in length
* 22809 22908: gap of unknown length
* 22909 24219: contig of 1311 bp in length
* 24220 24319: gap of unknown length
* 24320 25626: contig of 1307 bp in length
* 25627 25726: gap of unknown length
* 25727 28192: contig of 2466 bp in length
* 28193 28292: gap of unknown length
* 28293 29748: contig of 1456 bp in length
* 29749 29848: gap of unknown length
* 29849 32429: contig of 2581 bp in length
* 32430 32529: gap of unknown length
* 32530 34056: contig of 1527 bp in length
* 34057 34156: gap of unknown length
* 34157 36789: contig of 2633 bp in length
* 36790 36889: gap of unknown length
* 36890 38922: contig of 2033 bp in length
* 38923 39022: gap of unknown length
* 39023 41368: contig of 2346 bp in length
* 41369 41468: gap of unknown length

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* 41469	43309: contig of 1841 bp in length
* 43310	43409: gap of unknown length
* 43410	44931: contig of 1522 bp in length
* 44932	45031: gap of unknown length
* 45032	46557: contig of 1526 bp in length
* 46558	46557: gap of unknown length
* 46658	48429: contig of 1772 bp in length
* 48430	48429: gap of unknown length
* 48530	50022: contig of 1493 bp in length
* 50023	50122: gap of unknown length
* 50123	52297: contig of 2175 bp in length
* 52298	52397: gap of unknown length
* 52398	54714: contig of 2317 bp in length
* 54715	54814: gap of unknown length
* 54815	57089: contig of 2275 bp in length
* 57090	57189: gap of unknown length
* 57190	59531: contig of 2342 bp in length
* 59532	59631: gap of unknown length
* 59632	61794: contig of 2163 bp in length
* 61795	61894: gap of unknown length
* 61895	64800: contig of 2586 bp in length
* 64801	64800: gap of unknown length
* 64581	67569: contig of 2989 bp in length
* 67569	67669: gap of unknown length
* 67670	70830: contig of 3161 bp in length
* 70831	70930: gap of unknown length
* 70931	73573: contig of 2643 bp in length
* 73574	73673: gap of unknown length
* 73674	75900: contig of 2227 bp in length
* 75901	76000: gap of unknown length
* 76001	79411: contig of 3411 bp in length
* 79412	79511: gap of unknown length
* 79512	82590: contig of 3079 bp in length
* 82591	82690: gap of unknown length
* 82691	85441: contig of 2851 bp in length
* 85442	85641: gap of unknown length
* 85642	88575: contig of 2934 bp in length
* 88576	88675: gap of unknown length
* 88676	91359: contig of 2684 bp in length
* 91360	91459: gap of unknown length
* 91460	94169: contig of 2710 bp in length
* 94170	94269: gap of unknown length
* 94270	97967: contig of 3698 bp in length
* 97968	98067: gap of unknown length
* 98068	101121: contig of 3054 bp in length
* 101222	101221: gap of unknown length
* 104888	104888: contig of 3667 bp in length
* 104889	104988: gap of unknown length

Query Match 13.9% Score 35; DB 2; Length 230154;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

90 ACAAAAATCNCNNNNNNNNNNNNNNNNNNNNNNNN 124  
15338 ACAAAAATCNCNNNNNNNNNNNNNNNNNNNNNN 15372

RESULT 14  
AC094936/c  
AC094936/c  
Rattus norvegicus clone CH230-6E5, WORKING DRAFT SEQUENCE, 2  
AC094936 linear DNA 236385 bp HTG 09-MAY-2003  
unordered pieces.  
AC094936  
AC094936.6 GI:30466971  
HTG: HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 236385)  
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, W., Barnstead, M., Benham, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, M., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensu, L., Louised, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokeme, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puro, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrelle, R., Soea, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabak, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Temani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 236385)  
Worley, K.C.  
Direct Submission  
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 236385)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On May 9, 2003 this sequence version replaced gi:23101377.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome









82	29	11.6	2757	23	ABV24523	Human prostate exp	c 155	28	11.2	87	22	AAC84734	Nucleotide sequenc
83	29	11.6	3159	24	AA594918	Human DNA sequence	156	28	11.2	90	19	AAV39807	Anti-E4 RNA oligon
c 84	29	11.6	4336	8	AAV74857	Staphylococcus aur	157	28	11.2	90	24	ABK33906	Template DNA used
c 85	29	11.6	4438	9	AAAB2262	Alpha-2 plasmin in	c 158	28	11.2	91	22	AAF16661	DAMP specific apta
86	29	11.6	4708	6	AAAN50415	Human acetyl choli	159	28	11.2	93	14	AAQ39251	Platelet adhesi
87	29	11.6	4846	18	AAV74587	Staphylococcus aur	160	28	11.2	93	16	AAQ79694	Antisense oligonuc
88	29	11.6	4992	24	AA594783	Human DNA sequence	161	28	11.2	93	16	AAQ79087	Oligonucleotide en
89	29	11.6	5394	25	ACA303953	CDNA downregulated	162	28	11.2	93	19	AAV35010	Human endothelin-b
90	29	11.6	5727	18	AAV74501	Staphylococcus aur	163	28	11.2	93	21	AAA27010	Oligonucleotide fo
c 91	29	11.6	6346	18	AAV74548	Staphylococcus aur	c 164	28	11.2	94	18	AAAT94526	Gene library codin
c 92	29	11.6	6777	25	ABX63289	Human CDNA #289 di	c 165	28	11.2	94	20	AAAI5131	Coding sequence of
c 93	29	11.6	13999	14	AAO43845	Plasmid pAH4611.	166	28	11.2	94	22	AAAF3455	Hepatocyte growth
c 94	29	11.6	33780	22	AAH24652	Nucleotide sequenc	167	28	11.2	95	21	AAA93771	Adaptor used in me
95	29	11.6	45862	25	ABX93110	Genomic DNA encodi	168	28	11.2	96	18	AAAT5435	Platelet derived g
c 96	29	11.6	57699	25	ABV75538	Human transporter	169	28	11.2	96	20	AAAT87036	Starting RNA used
97	29	11.6	121001	21	AAV22284	BAC containing rep	170	28	11.2	97	18	AAAT58049	Template 50N8 for
98	29	11.6	487980	25	AA53223	Human chromosome 3	171	28	11.2	100	16	AAQ92421	Human HLA-DRB frag
99	28	11.2	49	24	ABK70501	In-situ analysis s	172	28	11.2	100	20	AAAT78167	T7 RNA polymerase
100	28	11.2	65	20	AA25202	SMAD4-FL binding o	173	28	11.2	104	19	AAV41760	Synthetic DNA temp
101	28	11.2	65	22	AA500220	Randomised oligonu	174	28	11.2	104	19	AAV43311	Randomised oligonu
c 102	28	11.2	70	21	AAAG60395	HLA class II DR A p	175	28	11.2	104	22	AAAF3640	HGF nucleic acid l
c 103	28	11.2	72	19	AAV39804	Anti-E4 RNA oligon	176	28	11.2	104	24	ABK31550	DNA template for c
c 104	28	11.2	72	24	ABK13903	DNA oligonucleotid	177	28	11.2	104	25	ABX80491	Nucleic acid ligan
105	28	11.2	73	17	AAAT71327	Red blood cell gho	c 178	28	11.2	107	16	AAAT06076	Template sequence
106	28	11.2	73	19	AAV39808	Anti-E4 RNA oligon	179	28	11.2	107	16	AAAT06079	RNA template from
107	28	11.2	73	24	ABK13907	RNA transcript use	c 180	28	11.2	107	21	AAA48470	Termamyl-like alph
108	28	11.2	76	16	AAQ98396	Template molecule	c 181	28	11.2	111	18	AAV77549	Staphylococcus aur
109	28	11.2	76	16	AAQ98163	VEGF RNA high affi	c 182	28	11.2	113	24	ABQ82152	Oligonucleotide li
110	28	11.2	76	22	AAAF70633	SELEX experiment s	c 183	28	11.2	113	24	ABSS2652	RNA aptamer oligon
111	28	11.2	76	24	AAAD44095	Synthetic DNA used	c 184	28	11.2	114	24	AA520468	Library oligonucle
112	28	11.2	77	15	AAQ63025	Template used in S	c 185	28	11.2	118	18	AAV75833	Staphylococcus aur
113	28	11.2	77	16	AAAT73196	Template sequence	c 186	28	11.2	119	14	AAQ48613	Synthetic antibody
114	28	11.2	77	16	AAQ89172	VEGF RNA high affi	c 187	28	11.2	123	24	ABA94828	Nucleotide sequenc
115	28	11.2	77	17	AAAT97615	Generic nucleic ac	188	28	11.2	124	24	ABA94841	Nucleotide sequenc
116	28	11.2	77	17	AAAT97689	First cycle start	189	28	11.2	147	20	AAAX01793	Oligonucleotide 10
117	28	11.2	77	18	AAV00778	Template for isola	c 190	28	11.2	147	21	AAAI3674	147 nucleotide 100
118	28	11.2	77	18	AAAT87305	30N ssDNA template	c 191	28	11.2	162	18	AAV75660	Staphylococcus aur
119	28	11.2	77	19	AAV14559	SELEX template for	c 192	28	11.2	204	18	AAV77458	Staphylococcus aur
120	28	11.2	77	20	AAAX01791	Oligonucleotide 30	c 193	28	11.2	217	24	ABK93423	Human breast speci
121	28	11.2	77	20	AAV79638	Starting RNA seque	194	28	11.2	233	24	AAAD28249	Human pancreatic t
122	28	11.2	77	21	AAAG27738	HSV-1 DNA polymera	195	28	11.2	236	24	ABL74465	Corn tassell-derive
123	28	11.2	77	21	AAAI3672	GMPS-RNA molecule	c 196	28	11.2	251	18	AAV78865	Staphylococcus aur
124	28	11.2	77	21	AA525749	Randomised nucleot	197	28	11.2	281	24	ABN87704	Human prostate spe
125	28	11.2	77	22	AAAF73456	Hepatocyte growth	c 198	28	11.2	283	25	ABX82525	Corn ear-derived p
126	28	11.2	77	22	AAAF70539	SELEX experiment o	199	28	11.2	284	24	ABL72867	Corn tassell-derive
127	28	11.2	77	24	ABK61114	SELEX process nucl	c 200	28	11.2	285	22	AAAL08943	Human breast cance
128	28	11.2	79	14	AAQ52392	Template RNA used	c 201	28	11.2	287	25	ABX87111	Corn ear-derived p
c 129	28	11.2	79	21	AAAI2100	T. brucei trypanos	c 202	28	11.2	311	23	ABV24993	Human prostate exp
c 130	28	11.2	80	24	AAAL48343	Cytohesin binding	c 203	28	11.2	322	23	ABV25624	Human prostate exp
c 131	28	11.2	82	20	AAAT78164	Selex procedure an	c 204	28	11.2	326	18	AAV77421	Staphylococcus aur
c 132	28	11.2	83	20	AAAT78162	Selex procedure ta	c 205	28	11.2	330	24	ABT03316	Ovary cell-specifi
c 133	28	11.2	83	20	AAAT78168	T7 RNA polymerase	c 206	28	11.2	337	12	AAQ12093	Pregnancy-specific
c 134	28	11.2	86	22	AAAD10615	JH101 oligo used i	207	28	11.2	339	24	AAAL3963	Lung-specific nucl
c 135	28	11.2	87	15	AAQ63023	Template used in S	208	28	11.2	341	23	AAAS2087	DNA encoding novel
c 136	28	11.2	87	16	AAQ89175	VEGF RNA high affi	209	28	11.2	351	18	AAV78652	Staphylococcus aur
137	28	11.2	87	17	AAAT42819	Oligonucleotide 40	c 210	28	11.2	351	18	AAV78389	Staphylococcus aur
138	28	11.2	87	17	AAAT28376	40N8 random sequen	c 211	28	11.2	362	22	AAI84424	Human polynucleoti
139	28	11.2	87	17	AAAT8378	40N1 random sequen	c 212	28	11.2	368	22	AAAL08035	Human breast cance
140	28	11.2	87	18	AAAT93776	Rous sarcoma virus	c 213	28	11.2	368	22	AAAL08035	Human breast cance
c 141	28	11.2	87	18	AAAT84602	DNA template for s	c 214	28	11.2	373	21	AAA98496	Human breast cance
142	28	11.2	87	18	AAAT87685	40N ssDNA template	c 215	28	11.2	374	22	AAAL11395	Vicuna PTEN/MMAC1
143	28	11.2	87	18	AAAT97173	40N8 ssDNA templat	c 216	28	11.2	382	22	AA543337	DNA encoding novel
c 144	28	11.2	87	18	AAAT79123	SELEX template use	c 217	28	11.2	389	18	AAV78201	Staphylococcus aur
c 145	28	11.2	87	18	AAAT78661	40N template, for	c 218	28	11.2	390	24	ABQ73825	Human bone marrow
c 146	28	11.2	87	18	AAAT65425	Transforming growt	c 219	28	11.2	391	22	AAAD17399	DNA encoding novel
147	28	11.2	87	18	AAAT65428	Transforming growt	220	28	11.2	398	23	AA565727	DNA encoding novel
148	28	11.2	87	19	AAV41761	Random sequence RN	c 221	28	11.2	398	23	AA591583	DNA encoding novel
149	28	11.2	87	19	AAV43312	Randomised oligonu	c 222	28	11.2	398	25	ABZ18330	Group III cDNA can
150	28	11.2	87	20	AAAT85097	Human fibrin ligan	c 223	28	11.2	399	18	AAV77682	Staphylococcus aur
151	28	11.2	87	20	AAAX01789	Oligonucleotide 40	c 224	28	11.2	400	18	AAV78203	Staphylococcus aur
152	28	11.2	87	21	AAAI33670	40N8 RNA pool rand	c 225	28	11.2	400	18	AAV78167	Staphylococcus aur
153	28	11.2	87	22	AAAF73759	HGF nucleic acid l	c 226	28	11.2	400	18	AAV78076	Staphylococcus aur
154	28	11.2	87	22	AAAF73760	HGF nucleic acid l	c 227	28	11.2	400	18	AAV77945	Staphylococcus aur

228	28	11.2	400	18	AAV77258	Staphylococcus aur	301	28	11.2	963	24	ABZ43156	Human GPCR polynuc
229	28	11.2	407	23	AA575914	DNA encoding novel	c 302	28	11.2	963	24	ABZ43156	Human GPCR polynuc
230	28	11.2	408	23	AA565726	DNA encoding novel	303	28	11.2	972	23	AA566748	DNA encoding novel
231	28	11.2	408	23	AA591582	DNA encoding novel	c 304	28	11.2	986	25	ABZ18486	Group III cDNA can
232	28	11.2	412	23	AA569064	DNA encoding novel	c 305	28	11.2	1003	18	AAV74634	Staphylococcus aur
233	28	11.2	414	18	AAV75283	Staphylococcus aur	306	28	11.2	1010	22	AAI89570	Human polynucleoti
234	28	11.2	418	22	AAU11525	Human breast cancer	307	28	11.2	1021	18	AAV74325	Staphylococcus aur
235	28	11.2	420	22	AAU183198	Human polynucleoti	c 308	28	11.2	1060	18	AAV74766	Staphylococcus aur
236	28	11.2	423	22	AA588918	Human cancer relat	c 309	28	11.2	1071	24	ABZ43147	Human GPCR polynuc
237	28	11.2	423	23	AA582916	DNA encoding novel	310	28	11.2	1072	24	ABK92515	Human prostate spe
238	28	11.2	429	23	AA589131	Human cancer relat	311	28	11.2	1090	24	ABK92515	Human prostate spe
239	28	11.2	432	22	AAU08519	Human breast cancer	312	28	11.2	1126	11	AAQ06974	Human follicle-sti
240	28	11.2	440	24	ABK93480	Human breast speci	c 313	28	11.2	1134	24	ABT07897	Human lung specifi
241	28	11.2	441	25	ABZ18234	Group III cDNA can	c 314	28	11.2	1139	23	AA587665	DNA encoding novel
242	28	11.2	450	23	AA588231	DNA encoding novel	c 315	28	11.2	1145	18	AAV75088	Staphylococcus aur
243	28	11.2	459	20	AAV84299	Wheat geminivirus	316	28	11.2	1157	24	AAK53293	Human eosinophili-m
244	28	11.2	462	20	AAV84300	Wheat geminivirus	317	28	11.2	1166	20	AAK88570	Human chromosome 1
245	28	11.2	464	23	AA568866	DNA encoding novel	318	28	11.2	1191	25	ABZ18419	Group III cDNA can
246	28	11.2	464	25	ACA571175	Human adipocyte Se	319	28	11.2	1200	24	ABK72649	Modified DNA encod
247	28	11.2	470	22	AAI192703	Human polynucleoti	c 320	28	11.2	1242	18	AAV74901	Staphylococcus aur
248	28	11.2	471	22	AAU10724	Human breast cancer	c 321	28	11.2	1257	18	AAV75030	Staphylococcus aur
249	28	11.2	476	18	AAV77886	Staphylococcus aur	c 322	28	11.2	1260	24	ABL52277	Human modified PHK
250	28	11.2	477	23	AA591524	DNA encoding novel	c 323	28	11.2	1280	22	AAAF80542	Receptor #30 parti
251	28	11.2	481	22	AAU111459	Human breast cancer	c 324	28	11.2	1308	18	AAV74387	Staphylococcus aur
252	28	11.2	483	22	AAU11282	Human breast cancer	325	28	11.2	1312	18	AAV74494	Staphylococcus aur
253	28	11.2	491	22	AAI69562	Human polynucleoti	c 326	28	11.2	1320	25	AA516674	Human cytochrome P
254	28	11.2	495	18	AAV75525	Staphylococcus aur	c 327	28	11.2	1320	25	AA516674	Human cytochrome P
255	28	11.2	498	23	AA572533	DNA encoding novel	c 328	28	11.2	1354	25	ABZ18320	Group III cDNA can
256	28	11.2	498	23	AA572567	DNA encoding novel	329	28	11.2	1373	18	AAV74820	Staphylococcus aur
257	28	11.2	498	23	AA581004	DNA encoding novel	330	28	11.2	1461	16	AAAT30576	Leuconostoc lactis
258	28	11.2	517	22	AAH72557	Human cervical can	c 331	28	11.2	1490	24	ABL54570	Rhodospirillum rDN
259	28	11.2	525	25	ABZ20427	Oncofetal cDNA se	c 332	28	11.2	1500	24	ABK14142	Human aminolevulin
260	28	11.2	531	22	AAK32668	Human bone marrow	c 333	28	11.2	1544	24	ABS71615	Legionella pneumop
261	28	11.2	531	22	AAI38463	Probe #7169 used t	c 334	28	11.2	1560	24	AA433682	Human interleukin
262	28	11.2	531	23	ABS32385	Human liver single	335	28	11.2	1609	24	AA594861	Human DNA sequence
263	28	11.2	531	24	ABS07462	Human genome-deriv	c 336	28	11.2	1680	24	ABK52231	Human Cy27A1 modi
264	28	11.2	548	22	AAU08030	Human breast cancer	c 337	28	11.2	1683	22	AA566921	Human amyloid prec
265	28	11.2	574	18	AAV74886	Staphylococcus aur	338	28	11.2	1782	16	AAAT03251	Pseudomonas mesoac
266	28	11.2	588	23	ABV60736	Human prostate exp	c 339	28	11.2	1788	18	AAV74701	Staphylococcus aur
267	28	11.2	590	22	AAU07880	Human breast cancer	c 340	28	11.2	1801	23	ABV21121	Human prostate exp
268	28	11.2	608	23	ABV50405	Human prostate exp	c 341	28	11.2	1801	23	ABV23347	Human prostate exp
269	28	11.2	609	24	ABK32487	Human prostate spe	c 342	28	11.2	1801	23	ABV25696	Human prostate exp
270	28	11.2	617	24	ABN89007	Human prostate spe	c 343	28	11.2	1801	23	ABV26963	Human prostate exp
271	28	11.2	635	22	AAI80602	Human polynucleoti	c 344	28	11.2	1812	12	AAQ11071	Chromosomal HindII
272	28	11.2	641	18	AAV75788	Staphylococcus aur	345	28	11.2	1814	18	AAV74769	Staphylococcus aur
273	28	11.2	654	18	AAV75491	Staphylococcus aur	346	28	11.2	1816	18	AAV74662	Staphylococcus aur
274	28	11.2	670	19	AAV43797	Staphylococcus aur	347	28	11.2	1910	24	ABZ35468	Human gene express
275	28	11.2	670	19	AAV43797	Sequence used in t	c 348	28	11.2	1941	24	ABZ35435	Human gene express
276	28	11.2	672	25	ABZ18301	Sequence used in t	349	28	11.2	1972	22	AAK52691	Human polynucleoti
277	28	11.2	682	18	AAV74751	Group III cDNA can	c 350	28	11.2	1975	22	AAH89873	Human bone marrow
278	28	11.2	693	22	AAU09069	Staphylococcus aur	c 351	28	11.2	1984	18	AAV74450	Staphylococcus aur
279	28	11.2	693	22	AAU09069	Human breast cancer	352	28	11.2	2040	24	AAH11513	Human beta-3-adren
280	28	11.2	738	14	AAQ48606	Sequence encoding	c 353	28	11.2	2141	22	AAH75061	Nucleotide sequenc
281	28	11.2	740	24	ABQ68622	Listeria monocytog	c 354	28	11.2	2146	25	ACA03962	cDNA downregulated
282	28	11.2	740	24	ABQ70070	Listeria monocytog	c 355	28	11.2	2148	24	AA594996	Human DNA sequence
283	28	11.2	756	24	AAU39964	Lung-specific nucl	356	28	11.2	2201	24	ABZ35346	Human gene express
284	28	11.2	760	18	AAV75133	Staphylococcus aur	c 357	28	11.2	2209	24	ABK14301	DNA encoding proli
285	28	11.2	760	22	AAI93329	Human polynucleoti	c 358	28	11.2	2343	18	AAV74468	Staphylococcus aur
286	28	11.2	762	22	AAI92185	Human polynucleoti	c 359	28	11.2	2365	18	AAV74406	Staphylococcus aur
287	28	11.2	774	24	ABQ70962	Listeria monocytog	360	28	11.2	2366	24	ABK14302	DNA encoding trp s
288	28	11.2	780	24	ABK14447	Modified version o	361	28	11.2	2400	24	ABK50461	Human caspase 5, a
289	28	11.2	821	22	AAH94043	Human breast cancer	c 362	28	11.2	2400	24	ABK50461	Human caspase 5, a
290	28	11.2	821	22	AAH94043	Human foetal cDNA	363	28	11.2	2409	21	AAZ30341	Partial sequence o
291	28	11.2	835	22	AAAF93182	cDNA encoding SRT	c 364	28	11.2	2518	18	AAV74680	Staphylococcus aur
292	28	11.2	840	24	ABK47980	Human small induci	365	28	11.2	2549	18	AAV74936	Staphylococcus aur
293	28	11.2	883	23	ABV19680	Human prostate exp	366	28	11.2	2569	18	AAV74385	Staphylococcus aur
294	28	11.2	886	18	AAV74856	Staphylococcus aur	367	28	11.2	2574	18	AAV74752	Staphylococcus aur
295	28	11.2	914	22	AAI85445	Human polynucleoti	c 368	28	11.2	2822	23	ABV22239	Human prostate exp
296	28	11.2	918	24	ABT03398	Ovary cell-specifi	c 369	28	11.2	2822	23	ABV23675	Human prostate exp
297	28	11.2	919	22	AAI87811	Human polynucleoti	c 370	28	11.2	2822	23	ABV28077	Human prostate exp
298	28	11.2	951	24	ABQ70259	Listeria monocytog	c 371	28	11.2	2822	23	ABV29539	Human prostate exp
299	28	11.2	958	22	AAI88868	Human polynucleoti	372	28	11.2	2848	24	ABZ35045	Human gene express
300	28	11.2	960	20	AAZ16277	Human gene express	c 373	28	11.2	2980	24	ABZ35345	Human gene express

374	28	11.2	3093	20	AA58284	Human methylothioad	447	28	11.2	19806	24	ABN89476	Human dehydrogenas
375	28	11.2	3083	25	ABX10818	DNA encoding rat m	c 448	28	11.2	21990	24	ABK50071	Human CYP 11a1 gen
376	28	11.2	3176	18	AAV74726	Staphylococcus aur	c 449	28	11.2	22243	18	AAV74475	Staphylococcus aur
377	28	11.2	3240	24	ABL52076	Human SLC18A2 mod1	c 450	28	11.2	22884	18	ABQ99649	Human membrane spa
378	28	11.2	3240	24	ABL52076	Human SLC18A2 mod1	c 451	28	11.2	23439	18	AAV74349	Staphylococcus aur
379	28	11.2	3240	24	ABL52076	Human SLC18A2 mod1	c 452	28	11.2	27754	24	ABQ72998	Human transporter
380	28	11.2	3600	14	AAQ41230	Gene encoding majo	c 453	28	11.2	30246	18	AAV74367	Staphylococcus aur
381	28	11.2	3675	24	ABK12468	Human B-Factor Pro	c 454	28	11.2	31766	24	AAAL50687	Human sulphate tra
382	28	11.2	3733	24	AA594816	Plasmid vector pGX	c 455	28	11.2	31766	24	AAAL50687	Human sulphate tra
383	28	11.2	3821	18	AAV74615	Staphylococcus aur	c 456	28	11.2	31814	25	AAAD22781	Human Ras-like pro
384	28	11.2	3821	18	AAV74615	Staphylococcus aur	c 457	28	11.2	32480	24	ABA94267	Human Ras-like pro
385	28	11.2	4021	25	ACA03936	Human prostate exp	c 458	28	11.2	34337	24	ABL55857	Adenovirus related
386	28	11.2	4021	25	ACA03936	Human prostate exp	c 459	28	11.2	46050	25	ABX13974	Human GABA transpo
387	28	11.2	4029	18	AAV74612	cDNA downregulated	c 460	28	11.2	62488	24	AAAD44981	Human Ras-like pro
388	28	11.2	4034	24	AA594906	Human activated T	c 461	28	11.2	67087	21	AAAF22280	Human EMRI splice
389	28	11.2	4035	24	ABZ35238	Human DNA sequence	c 462	28	11.2	69327	21	ABF22280	BAC containing rep
390	28	11.2	4151	23	ABV24466	Human gene express	c 463	28	11.2	73544	25	ABF55821	Human transporter
391	28	11.2	4394	24	ABZ35513	Human prostate exp	c 464	28	11.2	73544	25	ABF55821	Human transporter
392	28	11.2	4467	22	AA85085	Human gene express	c 465	28	11.2	93223	21	AAAF22282	Human transporter
393	28	11.2	4549	18	AAV74485	Atherosclerosis-as	c 466	28	11.2	114693	25	AAAD48308	BAC containing rep
394	28	11.2	4557	18	AAV74652	Staphylococcus aur	c 467	28	11.2	121001	21	AAAF22284	Human transporter
395	28	11.2	4576	25	ABX63703	Staphylococcus aur	c 468	28	11.2	215980	24	AAAL38337	BAC containing rep
396	28	11.2	4669	18	AAV74443	Human cDNA #703 di	c 469	28	11.2	249999	25	ABK80229	Complementary stra
397	28	11.2	4721	18	AAV74545	Staphylococcus aur	c 470	28	11.2	326014	24	ABK99296	Human tramdorin ge
398	28	11.2	4733	18	AAV74744	Staphylococcus aur	c 471	28	11.2	569571	25	AAAD33224	Human gene for nov
399	28	11.2	4832	18	AAV74500	Staphylococcus aur	c 472	28	11.2	569571	25	AAAD33224	Human chromosome 3
400	28	11.2	4854	18	AAV74417	Staphylococcus aur	c 473	28	11.2	786431	24	ABQ74964	Human kinase prote
401	28	11.2	5024	24	AA594874	Staphylococcus aur	c 474	28	11.2	786431	24	ABQ74964	Cleavage site of h
402	28	11.2	5097	22	AAH57447	Human DNA sequence	c 475	27	10.8	39	19	AAV44494	Cleavage site of h
403	28	11.2	5301	24	AA594869	Human lung cell ep	c 476	27	10.8	40	21	AAAC70152	Randomising oligon
404	28	11.2	5445	18	AAV74384	Human DNA sequence	c 477	27	10.8	48	24	AAAD40013	PCR primer for 5'
405	28	11.2	5532	18	AAV74841	Staphylococcus aur	c 478	27	10.8	61	21	AAAC70148	Anti-E4 RNA oligon
406	28	11.2	5763	18	AAV74816	Staphylococcus aur	c 479	27	10.8	66	18	AAV79491	Mouse histone H2B
407	28	11.2	5804	18	AAV74560	Staphylococcus aur	c 480	27	10.8	66	22	AAAF6908	Sequence containin
408	28	11.2	5895	18	AAV74312	Staphylococcus aur	c 481	27	10.8	70	24	ABL57073	Oligo #5 for cloni
409	28	11.2	5924	18	AAV74441	Staphylococcus aur	c 482	27	10.8	72	24	ABA01319	Pseudoknot oligonu
410	28	11.2	5966	18	AAV74333	Staphylococcus aur	c 483	27	10.8	72	13	AAQ21832	DNA oligonucleotid
411	28	11.2	6591	18	AAV77425	Staphylococcus aur	c 484	27	10.8	72	24	ABK13903	Red blood cell gho
412	28	11.2	6637	24	AA594962	Human DNA sequence	c 485	27	10.8	72	19	AAV39804	Anti-E4 RNA oligon
413	28	11.2	6876	18	AAV74497	Staphylococcus aur	c 486	27	10.8	72	22	AAAF6908	RNA transcript use
414	28	11.2	6876	18	AAV74497	Staphylococcus aur	c 487	27	10.8	72	22	AAAF6908	SELEX template mol
415	28	11.2	6970	25	ABZ24594	Mouse ovary-specif	c 488	27	10.8	72	24	AAI72773	Template molecule
416	28	11.2	7953	18	AAV74463	Staphylococcus aur	c 489	27	10.8	72	24	ABK13903	VEGF RNA high affi
417	28	11.2	7965	18	AAV74632	Staphylococcus aur	c 490	27	10.8	73	17	AAAT71327	76mer library form
418	28	11.2	8339	18	AAV74486	Staphylococcus aur	c 491	27	10.8	73	19	AAV39808	SELEX experiment s
419	28	11.2	8668	14	AAQ50433	Partial human geno	c 492	27	10.8	73	15	AAQ63025	Template used in S
420	28	11.2	8779	18	AAV74369	Staphylococcus aur	c 493	27	10.8	75	16	AAQ98305	Template sequence
421	28	11.2	9179	18	AAV74411	Staphylococcus aur	c 494	27	10.8	76	16	AAQ98306	VEGF RNA high affi
422	28	11.2	9280	18	AAV74442	Staphylococcus aur	c 495	27	10.8	76	16	AAQ98306	Generic nucleic ac
423	28	11.2	9310	18	AAV74627	Staphylococcus aur	c 496	27	10.8	76	21	AAZ39846	First cycle start
424	28	11.2	9834	18	AAV74348	Staphylococcus aur	c 497	27	10.8	76	22	AAAF70633	Template for isola
425	28	11.2	10182	18	AAV74427	Staphylococcus aur	c 498	27	10.8	77	15	AAQ63025	30N sRNA template
426	28	11.2	10758	18	AAV74532	Staphylococcus aur	c 499	27	10.8	77	16	AAAT73196	SELEX template for
427	28	11.2	11466	18	AAV74755	Staphylococcus aur	c 500	27	10.8	77	16	AAQ98172	Oligonucleotide 30
428	28	11.2	11544	22	AAQ91455	celz integration v	c 501	27	10.8	77	17	AAAT97615	Starting RNA seque
429	28	11.2	11544	24	ABK13045	celz integration v	c 502	27	10.8	77	17	AAAT97615	HSV-1 DNA polymera
430	28	11.2	11544	24	ABK13045	celz integration v	c 503	27	10.8	77	18	AAV00778	GMPS-RNA molecule
431	28	11.2	11992	20	AAZ24729	Mouse amyloid prec	c 504	27	10.8	77	18	AAAT87305	Randomised nucleot
432	28	11.2	11992	20	AAZ24729	Mouse amyloid prec	c 505	27	10.8	77	19	AAV14559	SELEX experiment o
433	28	11.2	12494	24	ABA01438	Streptococcus ther	c 506	27	10.8	77	20	AAV01791	SELEX process nucl
434	28	11.2	12718	24	ABK52229	cDNA encoding huma	c 507	27	10.8	77	20	AAV79638	Template RNA used
435	28	11.2	13059	18	AAV74531	Staphylococcus aur	c 508	27	10.8	77	21	AAA92738	Primer of the inve
436	28	11.2	13182	25	ABX15028	Human gene encodin	c 509	27	10.8	77	21	AAA13672	SELEX procedure an
437	28	11.2	13856	18	AAV74342	Staphylococcus aur	c 510	27	10.8	77	21	AAZ52749	Randomised oligonu
438	28	11.2	15249	18	AAV74413	Staphylococcus aur	c 511	27	10.8	77	22	AAAF73456	Selex procedure an
439	28	11.2	15347	24	ABA01437	Streptococcus ther	c 512	27	10.8	77	22	AAAF70539	Selex procedure an
440	28	11.2	16110	24	ABA01437	Streptococcus ther	c 513	27	10.8	77	22	AAAF70539	Selex procedure an
441	28	11.2	16592	18	AAV74364	Staphylococcus aur	c 514	27	10.8	78	14	AAQ52392	Selex procedure an
442	28	11.2	16826	18	AAV74357	Staphylococcus aur	c 515	27	10.8	78	19	AAV16706	Selex procedure an
443	28	11.2	16826	18	AAV74357	Staphylococcus aur	c 516	27	10.8	78	21	AAZ92120	Selex procedure an
444	28	11.2	18355	18	AAV74378	Staphylococcus aur	c 517	27	10.8	82	20	AAV78164	Selex procedure an
445	28	11.2	18613	18	AAV74423	Staphylococcus aur	c 518	27	10.8	82	20	ABQ81252	Selex procedure ta
446	28	11.2	19738	24	ABA01436	Streptococcus ther	c 519	27	10.8	83	20	AAV78162	Selex procedure ta

C 520	27	10.8	83	20	AAx78168	T7 RNA polymerase	593	27	10.8	131	23	ABL41605	Nucleotide sequenc
C 521	27	10.8	85	18	AAV76406	Staphylococcus aur	594	27	10.8	133	24	ABL40278	Anti-DNA antibody
C 522	27	10.8	86	22	AAO10615	JH101 oligo used i	C 595	27	10.8	137	18	AAV79044	Staphylococcus aur
C 523	27	10.8	87	15	AAQ63023	Template used in S	596	27	10.8	138	18	AAV77147	Staphylococcus aur
C 524	27	10.8	87	16	AAQ89175	VEGF RNA high affi	C 597	27	10.8	139	24	ABA01325	Pseudoknot oligonu
C 525	27	10.8	87	17	AAAT42819	Oligonucleotide 40	598	27	10.8	141	18	AAV79206	Staphylococcus aur
C 526	27	10.8	87	17	AAAT28376	30N1 random sequen	599	27	10.8	141	18	AAV79487	Adenosine or adeno
C 527	27	10.8	87	17	AAAT28378	30N1 random sequen	C 600	27	10.8	142	18	AAV79486	Adenosine or adeno
C 528	27	10.8	87	18	AAAT93776	Rous sarcoma virus	601	27	10.8	145	18	AAV75966	Staphylococcus aur
C 529	27	10.8	87	18	AAAT84602	DNA template for s	C 602	27	10.8	147	18	AAV75637	Staphylococcus aur
C 530	27	10.8	87	18	AAAT84602	40N ssDNA template	C 603	27	10.8	147	20	AAV01793	Oligonucleotide 10
C 531	27	10.8	87	18	AAAT87173	40N8 ssDNA template	C 604	27	10.8	147	20	AAV01794	Oligonucleotide 10
C 532	27	10.8	87	18	AAAT79123	SELEX template use	C 605	27	10.8	147	20	AAV01794	Oligonucleotide 10
C 533	27	10.8	87	18	AAAT78661	40N template, for	C 606	27	10.8	147	21	AAA13674	147 nucleotide 100
C 534	27	10.8	87	18	AAAT65425	Transforming growt	607	27	10.8	147	21	AAA13675	147 nucleotide 100
C 535	27	10.8	87	18	AAAT65428	Transforming growt	C 608	27	10.8	147	21	AAA13675	147 nucleotide 100
C 536	27	10.8	87	19	AAV41761	Random sequence RN	C 609	27	10.8	148	18	AAV77593	Staphylococcus aur
C 537	27	10.8	87	19	AAV43312	Randomised oligonu	610	27	10.8	156	20	AAV88213	Oligonucleotide pr
C 538	27	10.8	87	20	AAV85097	Human fibrin ligan	C 611	27	10.8	156	20	AAV88213	Oligonucleotide pr
C 539	27	10.8	87	20	AAV85097	Oligonucleotide 40	C 612	27	10.8	165	4	AAV30314	Sequence of portio
C 540	27	10.8	87	21	AAAL1670	40N8 RNA pool rand	C 613	27	10.8	165	5	AAV40294	Sequence of portio
C 541	27	10.8	87	22	AAV73759	HGF nucleic acid l	C 614	27	10.8	165	18	AAV75693	Staphylococcus aur
C 542	27	10.8	87	22	AAV73759	HGF nucleic acid l	C 615	27	10.8	171	21	AAZ56692	Red clover necroti
C 543	27	10.8	87	22	AAV84734	Nucleotide sequenc	C 616	27	10.8	179	22	AA184781	Human polynucleoti
C 544	27	10.8	88	18	AAV77761	Staphylococcus aur	C 617	27	10.8	193	24	ABQ73532	HPV-PTM related ol
C 545	27	10.8	90	19	AAV19807	Anti-E4 RNA oligon	C 618	27	10.8	199	19	AAV23176	Saccharomyces cere
C 546	27	10.8	90	19	AAV11329	PDR-47 D-Arginine	C 619	27	10.8	199	25	ACA56323	Human signalling p
C 547	27	10.8	90	24	ABK13906	Template DNA used	620	27	10.8	208	18	AAV79488	Adenosine or adeno
C 548	27	10.8	92	16	AAQ83452	Template oligonucl	C 621	27	10.8	208	18	AAV79488	Adenosine or adeno
C 549	27	10.8	92	18	AAAT36331	Feline immunodefici	622	27	10.8	214	8	AAV71331	Exon 3 human chrom
C 550	27	10.8	92	18	AAAT36331	Feline immunodefici	C 623	27	10.8	215	24	ABK92416	Human prostate spe
C 551	27	10.8	92	20	AAV88045	Ku protein binding	624	27	10.8	222	6	AAV50752	Sequence of the hu
C 552	27	10.8	92	20	AAV88045	Ku protein binding	C 625	27	10.8	222	6	AAV50752	Sequence of the hu
C 553	27	10.8	92	24	AAAD30602	{AT}4-40N18-(A)8,	C 626	27	10.8	231	24	ABA01284	HIV-1 oligonucleot
C 554	27	10.8	92	24	AAAD30602	{AT}4-40N18-(A)8,	C 627	27	10.8	233	24	ABL75970	Corn tassal-derive
C 555	27	10.8	94	22	AAV73455	Hepatocyte growth	C 628	27	10.8	235	22	AAAL10146	Human breast cance
C 556	27	10.8	96	18	AAV65435	Platelet derived g	C 629	27	10.8	236	25	ABQ82915	Human lung specifi
C 557	27	10.8	96	20	AAV87036	Starting RNA used	630	27	10.8	237	22	AAAL08493	Human breast cance
C 558	27	10.8	97	18	AAV58049	Template 50N8 for	C 631	27	10.8	238	23	ABV60620	Human prostate exp
C 559	27	10.8	97	24	AAAL45385	Ion-dependent deox	632	27	10.8	240	22	AAAL08779	Human breast cance
C 560	27	10.8	97	24	AAAL45385	RNA-cleaving deoxy	C 633	27	10.8	247	18	ABL71831	Corn tassal-derive
C 561	27	10.8	99	19	AAV60453	Oligonucleotide us	C 634	27	10.8	249	18	AAV78931	Staphylococcus aur
C 562	27	10.8	99	24	AAAL48342	Cytohesin PCR prim	635	27	10.8	250	18	AAV75569	Staphylococcus aur
C 563	27	10.8	99	24	AAV01289	SECIS element #4.	C 636	27	10.8	250	22	AAAL08845	Human breast cance
C 564	27	10.8	100	18	AAV06063	DNA template for u	637	27	10.8	252	25	ABX83328	Exon 5 human chrom
C 565	27	10.8	100	20	AAZ23606	Template primer DN	C 638	27	10.8	264	8	AAV71333	Corn ear-derived p
C 566	27	10.8	100	20	AAZ23606	T7 RNA polymerase	639	27	10.8	265	25	ABX81751	Corn ear-derived p
C 567	27	10.8	101	16	AAQ93245	Random RNA templ	640	27	10.8	268	25	ABX82644	Corn ear-derived p
C 568	27	10.8	102	18	AAV77044	Staphylococcus aur	C 641	27	10.8	269	18	AAV78808	Staphylococcus aur
C 569	27	10.8	103	24	ABL51893	Nucleic acid senso	C 642	27	10.8	269	18	AAV75643	Staphylococcus aur
C 570	27	10.8	104	18	AAV79158	Staphylococcus aur	C 643	27	10.8	270	22	AAI89657	Human polynucleoti
C 571	27	10.8	104	19	AAV41760	Synthetic DNA temp	C 644	27	10.8	270	22	AAI90145	Human polynucleoti
C 572	27	10.8	104	19	AAV43311	Randomised oligonu	645	27	10.8	271	25	ABX81918	Corn ear-derived p
C 573	27	10.8	104	22	AAV73640	HGF nucleic acid l	646	27	10.8	275	22	AAI84880	Human polynucleoti
C 574	27	10.8	104	24	ABK31550	DNA template for c	647	27	10.8	279	25	ABX84949	Corn ear-derived p
C 575	27	10.8	104	25	ABX80491	Nucleic acid ligan	648	27	10.8	282	24	ABL74016	Corn tassal-derive p
C 576	27	10.8	107	16	AAV06076	Template sequence	649	27	10.8	282	25	ABX83778	Corn ear-derived p
C 577	27	10.8	107	16	AAV06079	RNA template from	C 650	27	10.8	282	25	ABX85720	Corn ear-derived p
C 578	27	10.8	107	17	AAAT34901	Single stranded DN	C 651	27	10.8	282	25	ABV93939	Human colon specif
C 579	27	10.8	107	20	AAV82944	Enzymatic oligo 107m	C 652	27	10.8	284	24	ABN87653	Human prostate spe
C 580	27	10.8	107	21	AAV92244	Synthetic oligomer	C 653	27	10.8	285	22	AAAL08943	Human breast cance
C 581	27	10.8	113	24	ABQ82152	Oligonucleotide li	C 654	27	10.8	285	23	ABV19903	Human prostate exp
C 582	27	10.8	113	24	ABSS2652	RNA aptamer oligon	655	27	10.8	290	24	ABL71025	Corn tassal-derive
C 583	27	10.8	114	18	AAV75798	Staphylococcus aur	656	27	10.8	292	25	ABX82351	Corn ear-derived p
C 584	27	10.8	114	24	AAAS20468	Library oligonucle	C 657	27	10.8	296	23	AAI81570	Human polynucleoti
C 585	27	10.8	116	24	AAAL43035	Regulatable, catal	C 658	27	10.8	296	23	AAAS85636	DNA encoding novel
C 586	27	10.8	118	18	AAV75666	Staphylococcus aur	659	27	10.8	297	22	AAAL08856	Human breast cance
C 587	27	10.8	123	18	AAV77224	Staphylococcus aur	C 660	27	10.8	299	20	AAV98276	Human cancer cell
C 588	27	10.8	124	21	AAZ44035	Construct 5' CAEV-	C 661	27	10.8	299	20	AAV98276	Human cancer cell
C 589	27	10.8	124	24	ABA94841	Nucleotide sequenc	662	27	10.8	299	22	AAI91740	Human polynucleoti
C 590	27	10.8	130	18	AAV77204	Staphylococcus aur	663	27	10.8	303	22	AAAL25388	Human breast cance
C 591	27	10.8	130	23	ABLS2908	Sialyl lewis-rela	C 664	27	10.8	303	22	AAAL25388	Human breast cance
C 592	27	10.8	130	23	ABLS4860	Cholesterol specif	C 665	27	10.8	303	25	ABX87363	Corn ear-derived p

666	27	10.8	304	22	AAL07642	Human breast cancer	c 739	27	10.8	394	18	AAV78194	Staphylococcus aur
667	27	10.8	304	22	AAL07642	Human breast cancer	c 740	27	10.8	395	21	AAF14421	Aspergillus oryzae
668	27	10.8	305	25	ABX87415	Corn ear-derived p	c 741	27	10.8	395	22	AAS59135	Human cancer relat
669	27	10.8	317	18	AAV75426	Staphylococcus aur	c 742	27	10.8	395	23	ABV24133	Human prostate exp
670	27	10.8	321	18	AAV75749	Staphylococcus aur	c 743	27	10.8	395	23	ABV29778	Human prostate exp
671	27	10.8	321	18	AAV75479	Staphylococcus aur	c 744	27	10.8	396	22	AAS59148	Human cancer relat
672	27	10.8	324	18	AAV78594	Staphylococcus aur	c 745	27	10.8	397	22	AAO09123	Human breast cancer
673	27	10.8	324	22	AAI93664	Human polynucleoti	c 746	27	10.8	397	23	ABV18183	Human prostate exp
674	27	10.8	324	23	AAS68328	DNA encoding novel	c 747	27	10.8	397	23	AAV585438	DNA encoding novel
675	27	10.8	325	18	AAV78640	Staphylococcus aur	c 748	27	10.8	398	14	AAQ51194	Plasmilar gene, U
676	27	10.8	326	18	AAV78835	Staphylococcus aur	c 749	27	10.8	399	18	AAV77304	Staphylococcus aur
677	27	10.8	327	18	AAV75476	Staphylococcus aur	c 750	27	10.8	399	18	AAV75654	Staphylococcus aur
678	27	10.8	333	18	AAV78701	Staphylococcus aur	c 751	27	10.8	400	18	AAV78299	Staphylococcus aur
679	27	10.8	333	18	AAV75337	Staphylococcus aur	c 752	27	10.8	400	18	AAV78283	Staphylococcus aur
680	27	10.8	334	22	AAI87593	Human polynucleoti	c 753	27	10.8	400	18	AAV78260	Staphylococcus aur
681	27	10.8	336	15	AAQ70086	DNA encoding MAb 1	c 754	27	10.8	400	18	AAV78212	Staphylococcus aur
682	27	10.8	337	23	ABV23161	Human prostate exp	c 755	27	10.8	400	18	AAV78190	Staphylococcus aur
683	27	10.8	337	23	ABV29001	Human prostate exp	c 756	27	10.8	400	18	AAV78174	Staphylococcus aur
684	27	10.8	337	23	AAV76170	DNA encoding novel	c 757	27	10.8	400	18	AAV78176	Staphylococcus aur
685	27	10.8	338	18	AAV78601	Staphylococcus aur	c 758	27	10.8	400	18	AAV78156	Staphylococcus aur
686	27	10.8	338	18	AAV78526	Staphylococcus aur	c 759	27	10.8	400	18	AAV78165	Staphylococcus aur
687	27	10.8	338	23	ABV54264	Human prostate exp	c 760	27	10.8	400	18	AAV78142	Staphylococcus aur
688	27	10.8	340	18	AAV77402	Staphylococcus aur	c 761	27	10.8	400	18	AAV78133	Staphylococcus aur
689	27	10.8	343	22	AAL08552	Human breast cancer	c 762	27	10.8	400	18	AAV78110	Staphylococcus aur
690	27	10.8	345	20	AAQ21044	Human NEWM antibod	c 763	27	10.8	400	18	AAV78117	Staphylococcus aur
691	27	10.8	345	24	ABX12526	DNA template for c	c 764	27	10.8	400	18	AAV78099	Staphylococcus aur
692	27	10.8	348	18	AAV78550	Staphylococcus aur	c 765	27	10.8	400	18	AAV78085	Staphylococcus aur
693	27	10.8	350	23	ABV30283	Human prostate exp	c 766	27	10.8	400	18	AAV78029	Staphylococcus aur
694	27	10.8	351	18	AAV76126	Staphylococcus aur	c 767	27	10.8	400	18	AAV78000	Staphylococcus aur
695	27	10.8	352	23	AAS93514	DNA encoding novel	c 768	27	10.8	400	18	AAV78002	Staphylococcus aur
696	27	10.8	354	25	ABZ18556	Group III cDNA can	c 769	27	10.8	400	18	AAV77980	Staphylococcus aur
697	27	10.8	357	22	AAI11352	Human breast cancer	c 770	27	10.8	400	18	AAV77982	Staphylococcus aur
698	27	10.8	359	23	AAV77752	DNA encoding novel	c 771	27	10.8	400	18	AAV77954	Staphylococcus aur
699	27	10.8	359	23	AAV78872	DNA encoding novel	c 772	27	10.8	400	18	AAV77918	Staphylococcus aur
700	27	10.8	360	24	ABX12100	Human interferon-g	c 773	27	10.8	400	18	AAV77893	Staphylococcus aur
701	27	10.8	360	25	ABV76206	Nicotinamide N-met	c 774	27	10.8	400	18	AAV77859	Staphylococcus aur
702	27	10.8	363	18	AAV79002	Staphylococcus aur	c 775	27	10.8	400	18	AAV76748	Staphylococcus aur
703	27	10.8	363	22	AAI82131	Human polynucleoti	c 776	27	10.8	400	18	AAV76692	Staphylococcus aur
704	27	10.8	364	23	ABV56939	Human prostate exp	c 777	27	10.8	400	18	AAV76420	Staphylococcus aur
705	27	10.8	364	25	ABX91943	Human G protein-co	c 778	27	10.8	400	18	AAV76366	Staphylococcus aur
706	27	10.8	365	22	AAS58961	Human cancer relat	c 779	27	10.8	400	18	AAV78545	Staphylococcus aur
707	27	10.8	367	18	AAV78401	Staphylococcus aur	c 780	27	10.8	400	18	AAV78545	Staphylococcus aur
708	27	10.8	370	22	AAL08266	Human breast cancer	c 781	27	10.8	400	18	AAV78514	Staphylococcus aur
709	27	10.8	370	24	ABK92401	Human prostate spe	c 782	27	10.8	400	18	AAV78464	Staphylococcus aur
710	27	10.8	373	21	AAV98496	Vicuna PTEN/MMAC1	c 783	27	10.8	400	18	AAV78427	Staphylococcus aur
711	27	10.8	374	22	AAL08328	Human breast cancer	c 784	27	10.8	400	18	AAV78436	Staphylococcus aur
712	27	10.8	374	22	AAI11395	Human breast cancer	c 785	27	10.8	400	18	AAV78436	Staphylococcus aur
713	27	10.8	374	22	AAI91055	Human polynucleoti	c 786	27	10.8	400	18	AAV78394	Staphylococcus aur
714	27	10.8	375	8	AAV71112	Sequence of PstI f	c 787	27	10.8	400	18	AAV78350	Staphylococcus aur
715	27	10.8	375	18	AAV78357	Staphylococcus aur	c 788	27	10.8	400	18	AAV78350	Staphylococcus aur
716	27	10.8	375	24	AAL53485	RNase P RNA region	c 789	27	10.8	400	18	AAV78329	Staphylococcus aur
717	27	10.8	377	18	AAV78311	Staphylococcus aur	c 790	27	10.8	400	23	AAV83174	DNA encoding novel
718	27	10.8	377	23	ABV19383	Human prostate exp	c 791	27	10.8	400	23	AAV85302	DNA encoding novel
719	27	10.8	379	18	AAV76517	Staphylococcus aur	c 792	27	10.8	400	23	AAV85302	DNA encoding novel
720	27	10.8	379	23	ABV16745	Human prostate exp	c 793	27	10.8	403	22	AAV59130	Human cancer relat
721	27	10.8	380	18	AAV78457	Staphylococcus aur	c 794	27	10.8	403	25	ACA57262	Human cancer relat
722	27	10.8	380	18	AAV78387	Staphylococcus aur	c 795	27	10.8	404	22	AAV59108	Human cancer relat
723	27	10.8	381	23	AAV18844	Human prostate exp	c 796	27	10.8	404	22	AAV59145	Human cancer relat
724	27	10.8	383	18	AAV78613	Staphylococcus aur	c 797	27	10.8	404	24	ABK93122	Human prostate spe
725	27	10.8	385	18	AAV78613	Staphylococcus aur	c 798	27	10.8	405	22	AAI80665	Human polynucleoti
726	27	10.8	385	22	AAI81278	Human polynucleoti	c 799	27	10.8	405	22	AAI81628	Human polynucleoti
727	27	10.8	386	18	AAV78373	Staphylococcus aur	c 800	27	10.8	407	22	AAV59889	Human novel cytoki
728	27	10.8	386	18	AAV78373	Staphylococcus aur	c 801	27	10.8	407	22	AAI11209	Human breast cancer
729	27	10.8	388	22	AAV43398	DNA encoding novel	c 802	27	10.8	407	23	AAV84914	DNA encoding novel
730	27	10.8	388	22	AAI83763	Human polynucleoti	c 803	27	10.8	408	23	AAV73120	DNA encoding novel
731	27	10.8	388	23	AAS83299	DNA encoding novel	c 804	27	10.8	411	22	AAI89090	Human polynucleoti
732	27	10.8	389	22	AAS58886	Human cancer relat	c 805	27	10.8	412	22	AAI83776	Human polynucleoti
733	27	10.8	389	23	AAV84418	DNA encoding novel	c 806	27	10.8	412	23	AAV66497	DNA encoding novel
734	27	10.8	390	25	ABZ71627	Breast specific nu	c 807	27	10.8	414	23	AAV67104	DNA encoding novel
735	27	10.8	391	22	AAS59156	Human cancer relat	c 808	27	10.8	415	22	AAI08319	Human breast cancer
736	27	10.8	391	23	AAV51523	DNA encoding novel	c 809	27	10.8	415	22	AAI08591	Human breast cancer
737	27	10.8	393	22	AAI83186	Human polynucleoti	c 810	27	10.8	415	22	AAI85235	Human polynucleoti
738	27	10.8	393	23	AAS81263	DNA encoding novel	c 811	27	10.8	415	25	ACA57236	Human adipocyte Se

812	27	10.8	416	23	AA586940	DNA encoding novel	c 885	27	10.8	464	23	ABV17986	Human prostate exp
813	27	10.8	416	23	AA587940	DNA encoding novel	c 886	27	10.8	464	23	AA568866	DNA encoding novel
814	27	10.8	417	22	AA184628	Human polynucleoti	c 887	27	10.8	465	6	AA50760	Sequence of the hu
815	27	10.8	417	23	AA567232	DNA encoding novel	c 888	27	10.8	467	25	ABZ71678	Breast specific nu
816	27	10.8	419	23	AA576367	DNA encoding novel	c 889	27	10.8	468	23	AA569012	DNA encoding novel
817	27	10.8	419	23	AA582743	DNA encoding novel	c 890	27	10.8	468	23	AA569012	DNA encoding novel
818	27	10.8	419	23	AA582766	DNA encoding novel	c 891	27	10.8	468	23	AA579790	DNA encoding novel
819	27	10.8	419	23	AA583980	DNA encoding novel	c 892	27	10.8	468	23	AA579790	DNA encoding novel
820	27	10.8	419	23	AA585103	DNA encoding novel	c 893	27	10.8	470	22	AA108280	Human breast cance
821	27	10.8	419	23	AA588114	DNA encoding novel	c 894	27	10.8	470	22	AA192703	Human polynucleoti
822	27	10.8	419	23	AA589461	DNA encoding novel	c 895	27	10.8	471	22	AA180595	Human polynucleoti
823	27	10.8	419	23	AA589585	DNA encoding novel	c 896	27	10.8	476	23	AA565767	DNA encoding novel
824	27	10.8	421	18	AAV79558	Staphylococcus aur	c 897	27	10.8	480	18	AAV78045	Staphylococcus aur
825	27	10.8	421	22	AA109104	Human breast cance	c 898	27	10.8	483	23	AA569581	DNA encoding novel
826	27	10.8	421	23	AA568848	DNA encoding novel	c 899	27	10.8	486	23	AA565480	DNA encoding novel
827	27	10.8	422	22	AA567309	Novel human polynu	c 900	27	10.8	487	24	AA139983	Lung-specific nucl
828	27	10.8	423	22	AA164895	Xanthomonas hrfl p	c 901	27	10.8	488	22	AA188888	Human polynucleoti
829	27	10.8	423	22	AA565593	DNA encoding novel	c 902	27	10.8	490	22	AA188885	Human polynucleoti
830	27	10.8	424	23	AA572383	DNA encoding novel	c 903	27	10.8	490	23	ABV18701	Human prostate exp
831	27	10.8	424	23	AA587647	DNA encoding novel	c 904	27	10.8	490	23	AA587979	DNA encoding novel
832	27	10.8	426	23	AA568333	DNA encoding novel	c 905	27	10.8	493	22	AA568095	Human lung tumour
833	27	10.8	427	24	AA591372	Human breast speci	c 906	27	10.8	493	24	ABK38006	cDNA encoding clon
834	27	10.8	428	22	AA108981	Human breast cance	c 907	27	10.8	493	25	ACA10335	Human lung cancer-
835	27	10.8	429	22	AA559154	Human cancer relat	c 908	27	10.8	493	25	ABX99286	Lung cancer therap
836	27	10.8	429	22	AA184007	Human polynucleoti	c 909	27	10.8	494	18	AAV78322	Staphylococcus aur
837	27	10.8	430	22	AA110892	Human breast cance	c 910	27	10.8	495	22	AA187721	Human polynucleoti
838	27	10.8	433	22	AA108819	Human breast cance	c 911	27	10.8	496	24	ABQ73822	Human colon specifi
839	27	10.8	434	23	AA570099	DNA encoding novel	c 912	27	10.8	498	23	AA572533	DNA encoding novel
840	27	10.8	434	24	ABL98893	Omega-conopeptide	c 913	27	10.8	498	23	AA572567	DNA encoding novel
841	27	10.8	435	23	AA589454	DNA encoding novel	c 914	27	10.8	498	23	AA581004	DNA encoding novel
842	27	10.8	436	18	AAV75752	Staphylococcus aur	c 915	27	10.8	501	18	AAV74965	Staphylococcus aur
843	27	10.8	436	23	AA564836	DNA encoding novel	c 916	27	10.8	503	24	ABK53643	Human eosinophil-m
844	27	10.8	436	23	AA579231	DNA encoding novel	c 917	27	10.8	511	22	AA593225	cDNA encoding SRT
845	27	10.8	436	23	AA583912	DNA encoding novel	c 918	27	10.8	511	24	ABK53647	Human eosinophil-m
846	27	10.8	436	23	AA584547	DNA encoding novel	c 919	27	10.8	512	23	ABV16864	Human prostate exp
847	27	10.8	436	23	AA581478	DNA encoding novel	c 920	27	10.8	514	18	AAV75344	Staphylococcus aur
848	27	10.8	437	22	AA181405	Human polynucleoti	c 921	27	10.8	514	23	ABV18541	Human prostate exp
849	27	10.8	437	23	ABV58188	Human prostate exp	c 922	27	10.8	516	21	AA98502	Quail PTEN/MMAC1 1
850	27	10.8	438	23	AA573611	DNA encoding novel	c 923	27	10.8	516	23	ABV25904	Human prostate exp
851	27	10.8	438	23	AA575599	DNA encoding novel	c 924	27	10.8	516	23	ABV25905	Human prostate exp
852	27	10.8	438	23	AA576938	DNA encoding novel	c 925	27	10.8	516	23	ABV29948	Human prostate exp
853	27	10.8	438	23	AA583175	DNA encoding novel	c 926	27	10.8	517	23	ABV24067	Human prostate exp
854	27	10.8	438	25	ABZ18200	Group III cDNA can	c 927	27	10.8	519	22	AA186819	Human polynucleoti
855	27	10.8	440	24	ABQ59714	Human colon cancer	c 928	27	10.8	520	22	AA193082	Human polynucleoti
856	27	10.8	441	23	AA583978	DNA encoding novel	c 929	27	10.8	524	23	ABV16560	Human prostate exp
857	27	10.8	441	23	AA588169	DNA encoding novel	c 930	27	10.8	524	23	ABV13795	Human prostate exp
858	27	10.8	441	23	AA589460	DNA encoding novel	c 931	27	10.8	524	23	ABV55409	Human prostate exp
859	27	10.8	442	23	AA575343	DNA encoding novel	c 932	27	10.8	527	24	ABQ92829	Triticum tauschii/
860	27	10.8	442	23	AA587088	DNA encoding novel	c 933	27	10.8	531	23	ABV19061	Human prostate exp
861	27	10.8	444	23	AA591551	DNA encoding novel	c 934	27	10.8	531	23	ABV21169	Human prostate exp
862	27	10.8	445	22	AA108420	Human breast cance	c 935	27	10.8	531	23	ABV26983	Human prostate exp
863	27	10.8	445	22	AA108583	Human prostate cance	c 936	27	10.8	532	22	ABA09461	Human adapter prot
864	27	10.8	447	23	ABV19306	Human adipocyte exp	c 937	27	10.8	535	18	AAV75767	Staphylococcus aur
865	27	10.8	447	25	ACA57254	Human adipocyte Se	c 938	27	10.8	535	24	ABK53467	Human eosinophil-m
866	27	10.8	448	23	ABV18787	Human prostate exp	c 939	27	10.8	542	23	AA582990	DNA encoding novel
867	27	10.8	448	23	ABV18927	Human prostate exp	c 940	27	10.8	542	23	AA582990	DNA encoding novel
868	27	10.8	448	23	AA580440	DNA encoding novel	c 941	27	10.8	544	24	ABK97867	Rat ARP-2 cDNA var
869	27	10.8	448	23	AA588157	DNA encoding novel	c 942	27	10.8	551	18	AAV75767	Staphylococcus aur
870	27	10.8	451	18	AAV75120	Staphylococcus aur	c 943	27	10.8	551	23	AA584015	DNA encoding novel
871	27	10.8	451	18	AAV74934	Staphylococcus aur	c 944	27	10.8	552	24	ABK92454	Human prostate spe
872	27	10.8	451	22	AA187457	Human polynucleoti	c 945	27	10.8	554	23	ABV19318	Human prostate exp
873	27	10.8	451	23	AA584020	DNA encoding novel	c 946	27	10.8	555	23	ABV30269	Human prostate exp
874	27	10.8	452	23	AA578257	DNA encoding novel	c 947	27	10.8	558	18	AAV74434	Staphylococcus aur
875	27	10.8	453	23	ABV17869	Human prostate exp	c 948	27	10.8	560	18	AAV78596	Staphylococcus aur
876	27	10.8	454	19	AAV18860	cDNA for tarantula	c 949	27	10.8	562	23	ABV22543	Human prostate exp
877	27	10.8	454	23	AA566075	DNA encoding novel	c 950	27	10.8	562	23	ABV22547	Human prostate exp
878	27	10.8	455	22	AA108178	Human breast cance	c 951	27	10.8	562	23	ABV27155	Human prostate exp
879	27	10.8	455	23	AA584918	DNA encoding novel	c 952	27	10.8	562	23	ABV28358	Human prostate exp
880	27	10.8	459	23	AA582876	DNA encoding novel	c 953	27	10.8	562	23	ABV28362	Human prostate exp
881	27	10.8	460	18	AAV74987	Staphylococcus aur	c 954	27	10.8	563	23	ABV20012	Human prostate exp
882	27	10.8	463	22	AA576947	DNA encoding novel	c 955	27	10.8	563	23	ABV21336	Human prostate exp
883	27	10.8	463	22	AA108929	Human breast cance	c 956	27	10.8	565	23	AA568134	DNA encoding novel
884	27	10.8	463	23	ABV18369	Human prostate exp	c 957	27	10.8	568	23	ABV18869	Human prostate exp



members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polynucleotide encoding a polypeptide in the adipocyte cells, a recombinant host cell expressing at least one of the interacting polypeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences given in the specification (including its fragment or variant), a vector comprising the SID (RTM) polynucleotide, a recombinant host cell comprising the vector, a protein chip comprising the polypeptides and a record comprising all or part of the data, listed in the specification. The complex, polypeptides, polynucleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polynucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains (SID (RTM)) for screening drugs that modulate the protein interaction, thus exhibiting the therapeutic effect. The present sequence encodes a SID (prey) protein of the invention.

Sequence 409 BP: 71 A; 68 C; 69 G; 105 T; 96 other;

Sequence 409 BP; 71 A; 68 C; 69 G; 105 T; 96 other;

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Query Match      12.4%; Score 31; DB 25; Length 409;
Best Local Similarity 100.0%; Pred.No. 2.2e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3  
ABZ20367/c  
ABZ20367 standard; cDNA: 765 BP.

ABZ20367;  
23-JAN-2003 (first entry)

Oncofoetal cDNA sequence overexpressed in tumour tissue SEQ ID NO:2794.

Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen; immune response; virology; immunology; microbiology; molecular biology; recombinant DNA technology; gene; ss.

Homo sapiens.  
WO200278516-A

10-OCT-2002.

28-MAR-2002; 2002WO-US10421.

30-MAR-2001; 2001US-280255P.  
28-AUG-2001; 2001US-315563P.  
09-JAN-2002; 2002US-347313P.

A (CORI-) CORIXA CORP.

Wang T, Wang S, Bangur CS, Gaiger A;

WPI; 2003-058387/05.

New immunogenic polynucleotides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and recombinant DNA techniques -

Claim 1; SEQ ID 2794; 207pp; English.

AB017575 to AB020506 represent isolated polynucleotide (I) sequences, and ABP54446 to ABP54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene

therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, immunology, microbiology, molecular biology and recombinant DNA techniques.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct/sequences](http://ftp.wipo.int/pub/published/pct/sequences).

Sequence 765 BP; 211 A; 123 C; 106 G; 266 T; 59 other;

Query Match 12.4%; Score 31; DB 25; Length 765;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
Matches 31; Conservative 0; Mismatches 0; Indels

**Qy** 94 AAAATC  
124  
**Db** 282 AAAATC  
252

RESULT 4  
AAV99321/c  
ID AAV99321 standard; cDNA; 1075 BP.

AC AAV99321

DT 25-MAR-1999 (first entry)

DE GDNFR-alpha cDNA clone 2.

Human; glial cell-line derived neurotrophic factor receptor- $\alpha$ ; KW  
 GDNF- $\alpha$ ; glial cell line-derived neurotrophic factor; GDNF; KW  
 neurturin; signal transduction; dopaminergic nerve cell; KW  
 Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; KW  
 neurological disorder; diabetes; glaucoma; sensory neuron; KW  
 retinal ganglion cell degeneration; sensory neuropathy; KW  
 retinopathy; gene therapy; ss. KW

XX  
OS Homo sapiens.

Key	Location/Qualifiers
CDS	2..445
FT	/*tag= a

XX  
PN  
W09854213-A2.

AA PD 03-DEC-1998.

27-APR-1998; 98WO-US08486

PR 30-MAY-1997; 97US-0866354

PA (AMGE-) AMGEN INC.

PI Fox GM, Jing S, Wen D;

DR WPI; 1999-080806/07.  
DR P-DCOR; BAW84172

XX New isolated alia  
PT

PT used to develop products for treating e.g. improperly functioning  
PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease  
PT or amyotrophic lateral sclerosis

PS Example 6; Page 148-149; 318pp; English.

The present sequence represents a cDNA clone insert encoding a human glial cell-line derived neurotrophic factor receptor- $\alpha$  (GDNFR- $\alpha$ ). The protein is capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and mediating cell response to GDNF. GDNFR- $\alpha$  proteins are functionally characterized by the ability to bind GDNF and/or neurturin specifically, and to







KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;  
XX gene therapy; ss.

OS Homo sapiens.

PH Location/Qualifiers  
XX Key 540..1937  
FT CDS /\*tag= a  
FT /product= GDNF\_receptor

XX W09740152-A1.

XX 30-OCT-1997.

XX 15-APR-1997; 97WO-US06281.

XX 14-APR-1997; 97US-0837199.

XX 22-APR-1996; 96US-0015907.

XX 09-MAY-1996; 96US-0017221.

XX (AMGE-) AMGEN INC.

XX Fox GM, Jing S, Wen D;

XX WPI; 1997-535836/49.

XX P-PSDB; AAW35333.

XX Glial cell line derived neurotrophic factor receptor - useful to  
XX treat dopaminergic nerve cell disorders, e.g. Parkinson's and  
XX Alzheimer's disease

XX Claim 17; Pages 91-93; 196pp; English.

XX The present sequence encodes the human glial cell line-derived  
XX neurotrophic factor (GDNF) receptor, which can be used to treat  
XX dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's  
XX disease or amyotrophic lateral sclerosis, complications of diabetes  
XX and Huntington's disease and (optionally in combination with GDNF)  
XX glaucoma, retinal degeneration and hearing loss caused by injury to  
XX inner ear sensory neurons. The receptor can also be used to block  
XX unwanted GDNF activity, analyse GDNF related molecules and  
XX stabilise GDNF in pharmaceutical formulations. Receptor expressing  
XX cells, preferably transfected ex vivo, can be used similarly by  
XX implantation, and the use of the receptor cDNA in gene therapy is  
XX also contemplated. Probes based on the cDNA can be used to identify  
XX GDNF responsive cells and tissues, e.g. to identify patients who  
XX would benefit from GDNF therapy, and abnormalities in receptor  
XX expression, and to isolate molecules that form a complex with the  
XX cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor  
XX antibodies, oligonucleotides derived from the cDNA and animal  
XX models that overexpress the receptor can be used to study the  
XX biological function of GDNF, knockout transgenic animals can be  
XX used to detect GDNF dependent neurons or processes and the antibody  
XX can be used in immunoassays for the receptor. The receptor binds  
XX GDNF specifically and with high affinity, acting as part of a  
XX complex that mediates/enhances signal transduction by GDNF, i.e.  
XX increasing dopamine uptake in dopaminergic cells.

XX Sequence 2568 BP; 631 A; 662 C; 625 G; 607 T; 43 other;

Query Match 12.4%; Score 31; DB 18; Length 2568;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
|||||

Db 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNN 2270  
|||||

RESULT 9  
RAV99310/c  
ID AAV99310 standard; cDNA; 2568 BP.  
XX

AC AAV99310;

XX 25-MAR-1999 (first entry)

XX Glial cell-line derived neurotrophic factor receptor-alpha cDNA.

XX Human; glial cell-line derived neurotrophic factor receptor-alpha;

XX GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;

XX neurturin; signal transduction; dopaminergic nerve cell;

XX Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;

XX neurological disorder; diabetes; glaucoma; sensory neuron;

XX retinal ganglion cell degeneration; sensory neuropathy;

XX retinopathy; gene therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 540..1937

XX /\*tag= a

XX /product= GDNFR-alpha

XX W09854213-A2.

XX 03-DEC-1998.

XX 27-APR-1998; 98WO-US08486.

XX 30-MAY-1997; 97US-0866354.

XX (AMGE-) AMGEN INC.

XX Fox GM, Jing S, Wen D;

XX WPI; 1999-080806/07.

XX P-PSDB; AAW84183.

XX New isolated glial cell line-derived neurotrophic factor receptors -  
XX used to develop products for treating e.g. improperly functioning  
XX dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease  
XX or amyotrophic lateral sclerosis

XX Claim 17; Fig 1A-M; 318pp; English.

XX The present sequence encodes a human glial cell-line derived  
XX neurotrophic factor receptor-alpha (GDNFR-alpha). The protein is  
XX capable of complexing with glial cell line-derived neurotrophic  
XX factor (GDNF) and mediating cell response to GDNF. GDNFR-alpha  
XX proteins are functionally characterised by the ability to bind  
XX GDNF and/or neurturin specifically, and to act as part of a  
XX molecular complex which mediates or enhances the signal transduction  
XX affects of GDNF and/or neurturin. The proteins can be used for treating  
XX improperly functioning dopaminergic nerve cells, Parkinson's disease,  
XX Alzheimer's disease or amyotrophic lateral sclerosis. They can  
XX also be used for treating neurological disorders associated with  
XX diabetes, glaucoma or other diseases and conditions involving retinal  
XX ganglion cell degeneration, sensory neuropathy caused by injury to,  
XX insults to, or degeneration of, sensory neurons, pathological conditions,  
XX or disease or injury-related retinopathies. The products can also be used  
XX for detection, diagnosis, drug screening and gene therapy.

XX Sequence 2568 BP; 631 A; 662 C; 625 G; 607 T; 43 other;

Query Match 12.4%; Score 31; DB 20; Length 2568;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
|||||

Db 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNN 2270  
|||||

RESULT 1C  
RAV99312/c

D AAV99312 standard; cDNA; 3209 BP.  
X AAV99312;  
X 25-MAR-1999 (first entry)  
X Glial cell-line derived neurotrophic factor receptor-alpha cDNA clone.  
X Human; glial cell-line derived neurotrophic factor receptor-alpha;  
X GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;  
X neurturin; signal transduction; dopaminergic nerve cell;  
X Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;  
X neurological disorder; diabetes; glaucoma; sensory neuron;  
X retinal ganglion cell degeneration; sensory neuropathy;  
X retinopathy; gene therapy; ss.  
X Homo sapiens.  
X Key Location/Qualifiers  
X CDS 540..1937  
X /\*tag= a  
X  
X WO9854213-A2.  
X 03-DEC-1998.  
X 27-APR-1998; 98WO-US08486.  
X 30-MAY-1997; 97US-0866354.  
X (AMGE-) AMGEN INC.  
X Fox GM, Jing S, Wen D;  
X WPI; 1999-080806/07.  
X P-ESDB; AAW84165.  
X New isolated glial cell line-derived neurotrophic factor receptors -  
X used to develop products for treating e.g. improperly functioning  
X dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease  
X or amyotrophic lateral sclerosis  
X  
X Example 6; Page 124-127; 318pp; English.  
X The present sequence represents a cDNA clone insert encoding a  
X human glial cell-line derived neurotrophic factor receptor-alpha  
X (GDNFR-alpha). The protein is capable of complexing with glial  
X cell line-derived neurotrophic factor (GDNF) and mediating cell  
X response to GDNF. GDNFR-alpha proteins are functionally characterised  
X by the ability to bind GDNF and/or neurturin specifically, and to act  
X as part of a molecular complex which mediates or enhances the signal  
X transduction affects of GDNF and/or neurturin. The proteins can be used  
X for treating improperly functioning dopaminergic nerve cells,  
X Parkinson's disease, Alzheimer's disease or amyotrophic lateral  
X sclerosis. They can also be used for treating neurological disorders  
X associated with diabetes, glaucoma or other diseases and conditions  
X involving retinal ganglion cell degeneration, sensory neuropathy caused  
X by injury to, insults to, or degeneration of, sensory neurons,  
X pathological conditions, or disease or injury-related retinopathies.  
X The products can also be used for detection, diagnosis, drug screening  
X and gene therapy.  
X  
X Sequence 3209 BP; 822 A; 795 C; 756 G; 795 T; 41 other;  
X  
X Query Match 12.4%; Score 31; DB 20; Length 3209;  
X Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
X Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
X  
X 94 AAAATCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
X |||||  
X 2300 AAAATCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

RESULT 11  
AAV74334  
ID AAV74334 standard; DNA; 17310 BP.  
XX AC  
XX AAV74334;  
XX 16-MAR-1999 (first entry)  
XX Staphylococcus aureus contig SEQ ID #23.  
XX Computer readable medium; vaccine; S.aureus infection; immunodetection;  
XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
XX skin infection; surgical wound infection; scalded skin syndrome;  
XX toxic shock syndrome; ds.  
XX Staphylococcus aureus.  
XX Key Location/Qualifiers  
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XX the sequence listing in the specification. They  
XX are included to maintain the nucleotide numbering  
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XX the sequence listing in the specification. They  
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XX the sequence listing in the specification. They  
XX are included to maintain the nucleotide numbering  
XX given in the specification for this DNA sequence"  
XX  
XX misc\_feature 16921..16980







GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 03:47:44 ; Search time 50 Seconds  
(without alignments)  
2215.743 Million cell updates/sec

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Perfect score: 251  
Sequence: 1 ggtgcagttgtgacaca.....gtaagaaganatcaacgcag 251

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA:\*

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- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
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- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C	1	31	12.4	1075	4	US-08-837-199A-21	Sequence 21, Appl
C	2	31	12.4	1076	4	US-08-837-199A-46	Sequence 46, Appl
C	3	31	12.4	2157	4	US-08-837-199A-15	Sequence 15, Appl
C	4	31	12.4	2158	4	US-08-837-199A-43	Sequence 43, Appl
C	5	31	12.4	2568	4	US-08-837-199A-1	Sequence 1, Appl
C	6	31	12.4	3209	4	US-08-837-199A-5	Sequence 5, Appl
C	7	31	12.4	3209	4	US-08-837-199A-37	Sequence 37, Appl
C	8	30	12.0	780	4	US-09-867-915-27	Sequence 27, Appl
C	9	30	12.0	3017	4	US-09-484-970B-36	Sequence 26, Appl
C	10	29	11.6	42	4	US-08-679-493A-55	Sequence 55, Appl
C	11	29	11.6	1045	3	US-09-313-300-9	Sequence 9, Appl
C	12	29	11.6	13999	3	US-08-444-644-24	Sequence 24, Appl
C	13	29	11.6	13999	4	US-08-233-246A-24	Sequence 24, Appl
C	14	29	11.6	174493	4	US-09-804-471A-3	Sequence 31, Appl
C	15	28	11.2	65	4	US-09-645-629-31	Sequence 31, Appl
C	16	28	11.2	68	2	US-08-590-571-6	Sequence 6, Appl
C	17	28	11.2	70	3	US-08-906-691-1	Sequence 1, Appl
C	18	28	11.2	72	4	US-09-314-268-174	Sequence 174, App
C	19	28	11.2	73	1	US-08-434-001-1	Sequence 1, Appl
C	20	28	11.2	73	1	US-08-433-585-1	Sequence 1, Appl
C	21	28	11.2	73	1	US-08-434-425-1	Sequence 1, Appl
C	22	28	11.2	73	2	US-08-437-667-1	Sequence 1, Appl
C	23	28	11.2	73	3	US-08-906-955-1	Sequence 1, Appl
C	24	28	11.2	73	3	US-08-945-903-1	Sequence 1, Appl
C	25	28	11.2	73	4	US-09-314-268-178	Sequence 178, App
C	26	28	11.2	73	4	US-09-396-002A-1	Sequence 1, Appl
C	27	28	11.2	73	5	PCT-US96-06060-1	Sequence 1, Appl

76	1	US-08-384-708A-95	Sequence 95, Appl
76	1	US-08-447-169A-57	Sequence 57, Appl
76	3	US-08-233-012C-57	Sequence 57, Appl
76	3	US-08-687-421-95	Sequence 95, Appl
77	1	US-07-931-473B-38	Sequence 38, Appl
77	1	US-07-714-131C-38	Sequence 38, Appl
77	1	US-08-442-572-57	Sequence 57, Appl
77	1	US-08-399-412A-1	Sequence 1, Appl
77	1	US-08-384-708A-1	Sequence 1, Appl
77	1	US-08-412-110-38	Sequence 38, Appl
77	1	US-08-409-442A-38	Sequence 38, Appl
77	1	US-08-400-440A-1	Sequence 1, Appl
77	1	US-08-361-795-57	Sequence 57, Appl
77	1	US-08-463-093A-1	Sequence 1, Appl
77	2	US-08-447-169A-1	Sequence 1, Appl
77	2	US-08-469-609A-38	Sequence 38, Appl
77	2	US-08-233-012C-1	Sequence 1, Appl
77	2	US-08-618-700-4	Sequence 4, Appl
77	2	US-08-460-888A-1	Sequence 1, Appl
77	2	US-08-477-527A-206	Sequence 206, App
77	2	US-08-894-578-1	Sequence 1, Appl
77	3	US-08-481-710-206	Sequence 206, App
77	3	US-09-157-601-4	Sequence 4, Appl
77	3	US-09-143-190-38	Sequence 38, Appl
77	3	US-08-687-421-1	Sequence 1, Appl
77	4	US-09-412-017-1	Sequence 1, Appl
77	4	US-09-502-344-38	Sequence 38, Appl
77	4	US-09-364-539-6	Sequence 6, Appl
77	5	PCT-US95-05600-140	Sequence 140, App
77	5	PCT-US95-11982-4	Sequence 4, Appl
77	5	PCT-US96-09537-206	Sequence 206, App
87	1	US-08-199-507B-54	Sequence 54, Appl
87	1	US-08-243-870-2	Sequence 2, Appl
87	1	US-08-477-530-1	Sequence 1, Appl
87	1	US-08-477-530-1	Sequence 1, Appl
87	1	US-08-409-439A-2	Sequence 2, Appl
87	1	US-08-477-830-1	Sequence 1, Appl
87	1	US-08-433-126A-40	Sequence 40, Appl
87	1	US-08-309-245-2	Sequence 2, Appl
87	1	US-08-462-389-2	Sequence 2, Appl
87	1	US-08-458-423A-49	Sequence 49, Appl
87	1	US-08-458-423A-52	Sequence 52, Appl
87	1	US-08-458-424B-49	Sequence 49, Appl
87	1	US-08-458-424B-52	Sequence 52, Appl
87	1	US-08-441-828-54	Sequence 54, Appl
87	1	US-08-433-124A-40	Sequence 40, Appl
87	1	US-08-463-101-2	Sequence 2, Appl
87	1	US-08-591-989-12	Sequence 12, Appl
87	2	US-08-488-402A-64	Sequence 64, Appl
87	2	US-08-488-402A-79	Sequence 79, Appl
87	2	US-08-484-552A-64	Sequence 64, Appl
87	2	US-08-484-552A-79	Sequence 79, Appl
87	2	US-08-618-700-2	Sequence 2, Appl
87	2	US-08-799-949-2	Sequence 2, Appl
87	2	US-08-477-527A-74	Sequence 74, Appl
87	2	US-08-477-527A-186	Sequence 186, App
87	3	US-08-481-710-74	Sequence 74, Appl
87	3	US-08-481-710-186	Sequence 186, App
87	3	US-08-793-398-2	Sequence 2, Appl
87	3	US-08-793-398-4	Sequence 4, Appl
87	3	US-09-157-601-2	Sequence 2, Appl
87	3	US-08-976-413A-40	Sequence 40, Appl
87	3	US-08-973-124-49	Sequence 49, Appl
87	3	US-08-973-124-52	Sequence 52, Appl
87	3	US-09-335-012-44	Sequence 44, Appl
87	4	US-09-364-539-192	Sequence 192, App
87	4	US-09-941-964-44	Sequence 44, Appl
87	4	US-10-096-830-44	Sequence 44, Appl
87	5	PCT-US95-11982-2	Sequence 2, Appl
87	5	PCT-US95-11982A-2	Sequence 2, Appl
87	5	PCT-US96-06059-40	Sequence 40, Appl
87	5	PCT-US96-08014-49	Sequence 49, Appl



101	28	11.2	87	5	PCT-US96-08014-52	Sequence 52, Appl	174	27	10.8	46	4	US-08-912-951-301	Sequence 301, App
102	28	11.2	87	5	PCT-US96-09472-64	Sequence 64, Appl	175	27	10.8	52	3	US-08-974-549A-535	Sequence 535, App
103	28	11.2	87	5	PCT-US96-09472-79	Sequence 79, Appl	176	27	10.8	52	4	US-08-912-951-302	Sequence 302, App
104	28	11.2	87	5	PCT-US96-09537-74	Sequence 74, Appl	177	27	10.8	58	3	US-08-974-549A-536	Sequence 536, App
105	28	11.2	87	5	PCT-US96-09537-186	Sequence 186, App	178	27	10.8	58	4	US-08-912-951-303	Sequence 303, App
106	28	11.2	90	1	US-08-358-995-28	Sequence 28, Appl	179	27	10.8	61	3	US-09-275-850-344	Sequence 344, App
107	28	11.2	90	4	US-09-314-268-177	Sequence 177, App	c 180	27	10.8	61	3	US-09-275-850-345	Sequence 345, App
c 108	28	11.2	93	1	US-09-578-634A-5	Sequence 5, Appl	181	27	10.8	62	2	US-08-659-453B-4	Sequence 4, Appl
109	28	11.2	93	1	US-08-370-567-27	Sequence 27, Appl	182	27	10.8	62	2	US-09-089-853A-4	Sequence 4, Appl
110	28	11.2	93	1	US-08-438-759-27	Sequence 27, Appl	183	27	10.8	62	3	US-09-131-009A-4	Sequence 4, Appl
111	28	11.2	93	1	US-08-538-911-2	Sequence 2, Appl	184	27	10.8	62	3	US-09-092-226A-4	Sequence 4, Appl
112	28	11.2	93	1	US-08-117-361C-15	Sequence 15, Appl	185	27	10.8	62	3	US-09-130-862A-4	Sequence 4, Appl
113	28	11.2	93	5	PCT-US94-05591-2	Sequence 2, Appl	186	27	10.8	62	3	US-09-090-809A-4	Sequence 4, Appl
114	28	11.2	94	5	PCT-US94-05684-27	Sequence 27, Appl	187	27	10.8	62	4	US-09-053-116A-4	Sequence 4, Appl
c 115	28	11.2	94	4	US-08-771-201-6	Sequence 6, Appl	188	27	10.8	66	2	US-08-659-453B-1	Sequence 1, Appl
116	28	11.2	94	4	US-09-364-539-5	Sequence 36, Appl	189	27	10.8	66	3	US-09-089-853A-1	Sequence 1, Appl
117	28	11.2	96	1	US-08-479-783A-36	Sequence 36, Appl	190	27	10.8	66	3	US-09-131-009A-1	Sequence 1, Appl
118	28	11.2	96	1	US-08-479-725-36	Sequence 36, Appl	191	27	10.8	66	3	US-09-092-226A-1	Sequence 1, Appl
119	28	11.2	96	1	US-08-618-693-36	Sequence 36, Appl	192	27	10.8	66	3	US-09-130-862A-1	Sequence 1, Appl
120	28	11.2	96	3	US-08-973-124-135	Sequence 125, App	193	27	10.8	66	3	US-09-090-809A-1	Sequence 1, Appl
121	28	11.2	96	3	US-08-991-743C-36	Sequence 36, Appl	194	27	10.8	66	4	US-09-053-116A-1	Sequence 1, Appl
122	28	11.2	96	4	US-09-851-486-36	Sequence 36, Appl	195	27	10.8	72	2	US-07-829-461A-6	Sequence 6, Appl
123	28	11.2	96	5	PCT-US96-08014-125	Sequence 125, App	196	27	10.8	72	3	US-09-197-649-5	Sequence 5, Appl
124	28	11.2	97	1	US-08-447-172A-4	Sequence 1, Appl	197	27	10.8	72	4	US-08-679-493A-54	Sequence 54, Appl
125	28	11.2	97	1	US-08-447-172A-4	Sequence 4, Appl	198	27	10.8	72	4	US-09-314-268-174	Sequence 174, App
126	28	11.2	97	3	US-08-952-793-248	Sequence 248, App	c 199	27	10.8	73	1	US-08-434-001-1	Sequence 1, Appl
127	28	11.2	97	3	US-08-952-793-390	Sequence 390, App	c 200	27	10.8	73	1	US-08-433-585-1	Sequence 1, Appl
128	28	11.2	97	3	US-08-949-928-248	Sequence 248, App	c 201	27	10.8	73	1	US-08-434-425-1	Sequence 1, Appl
129	28	11.2	97	4	US-09-849-928-390	Sequence 390, App	c 202	27	10.8	73	2	US-08-437-667-1	Sequence 1, Appl
130	28	11.2	97	5	PCT-US96-09455A-248	Sequence 248, App	c 203	27	10.8	73	2	US-08-906-955-1	Sequence 1, Appl
131	28	11.2	97	5	PCT-US96-09455A-390	Sequence 390, App	c 204	27	10.8	73	3	US-08-945-909-1	Sequence 1, Appl
132	28	11.2	104	1	US-08-591-989-11	Sequence 11, Appl	c 205	27	10.8	73	4	US-09-314-268-178	Sequence 178, App
133	28	11.2	104	2	US-08-799-949-1	Sequence 1, Appl	c 206	27	10.8	73	4	US-09-396-002A-1	Sequence 1, Appl
134	28	11.2	104	4	US-09-364-543-1	Sequence 1, Appl	c 207	27	10.8	73	5	PCT-US96-06060-1	Sequence 1, Appl
c 135	28	11.2	104	4	US-09-364-539-191	Sequence 191, App	c 208	27	10.8	76	1	US-08-384-708A-95	Sequence 95, Appl
c 136	28	11.2	107	1	US-08-441-591-1	Sequence 1, Appl	c 209	27	10.8	76	1	US-08-447-169A-57	Sequence 57, Appl
137	28	11.2	107	1	US-08-441-591-4	Sequence 4, Appl	c 210	27	10.8	76	2	US-08-233-012C-57	Sequence 57, Appl
c 138	28	11.2	107	1	US-08-303-362A-1	Sequence 1, Appl	c 211	27	10.8	76	3	US-08-687-421-95	Sequence 95, Appl
139	28	11.2	107	1	US-08-303-362A-4	Sequence 4, Appl	c 212	27	10.8	76	3	US-09-287-936-1	Sequence 1, Appl
c 140	28	11.2	107	3	US-09-193-068-21	Sequence 21, Appl	c 213	27	10.8	77	1	US-07-931-473B-38	Sequence 38, Appl
141	28	11.2	107	5	PCT-US95-05600-18	Sequence 18, Appl	c 214	27	10.8	77	1	US-07-714-131C-38	Sequence 38, Appl
c 142	28	11.2	107	5	PCT-US95-05600-21	Sequence 21, Appl	c 215	27	10.8	77	1	US-08-442-572-57	Sequence 57, Appl
143	28	11.2	119	1	US-07-843-125-9	Sequence 9, Appl	c 216	27	10.8	77	1	US-08-399-412A-1	Sequence 1, Appl
144	28	11.2	147	2	US-08-618-700-6	Sequence 6, Appl	c 217	27	10.8	77	1	US-08-384-708A-1	Sequence 1, Appl
145	28	11.2	147	3	US-09-157-601-6	Sequence 6, Appl	c 218	27	10.8	77	1	US-08-412-110-38	Sequence 38, Appl
c 146	28	11.2	283	4	US-09-313-294A-985	Sequence 985, App	c 219	27	10.8	77	1	US-08-409-442A-38	Sequence 38, Appl
c 147	28	11.2	287	4	US-09-313-294A-5571	Sequence 5571, App	c 220	27	10.8	77	1	US-08-400-440A-17	Sequence 17, Appl
c 148	28	11.2	333	4	US-09-252-991A-38	Sequence 38, Appl	c 221	27	10.8	77	1	US-08-361-795-57	Sequence 57, Appl
c 149	28	11.2	463	4	US-09-612-473-42	Sequence 42, Appl	c 222	27	10.8	77	1	US-08-463-093A-1	Sequence 1, Appl
150	28	11.2	670	2	US-08-784-208-2	Sequence 2, Appl	c 223	27	10.8	77	1	US-08-447-169A-1	Sequence 1, Appl
c 151	28	11.2	670	2	US-08-784-208-2	Sequence 2, Appl	c 224	27	10.8	77	2	US-08-469-609A-38	Sequence 38, Appl
152	28	11.2	738	1	US-07-843-125-2	Sequence 2, Appl	c 225	27	10.8	77	2	US-08-233-012C-1	Sequence 1, Appl
c 153	28	11.2	750	3	US-08-821-994-40	Sequence 40, Appl	c 226	27	10.8	77	2	US-08-618-700-4	Sequence 4, Appl
154	28	11.2	1280	3	US-09-276-531-52	Sequence 52, Appl	c 227	27	10.8	77	2	US-08-460-888A-1	Sequence 1, Appl
155	28	11.2	1461	3	US-08-445-463B-5	Sequence 5, Appl	c 228	27	10.8	77	2	US-08-477-527A-206	Sequence 206, App
156	28	11.2	1461	3	US-08-445-464C-5	Sequence 5, Appl	c 229	27	10.8	77	2	US-08-894-578-1	Sequence 1, Appl
157	28	11.2	1461	4	US-08-044-857D-5	Sequence 5, Appl	c 230	27	10.8	77	3	US-08-481-710-206	Sequence 206, App
158	28	11.2	1461	5	PCT-US94-03437-5	Sequence 5, Appl	c 231	27	10.8	77	3	US-09-157-601-4	Sequence 4, Appl
159	28	11.2	1782	1	US-08-374-155A-13	Sequence 13, Appl	c 232	27	10.8	77	3	US-09-143-190-38	Sequence 38, Appl
160	28	11.2	1782	2	US-08-785-396-13	Sequence 13, Appl	c 233	27	10.8	77	3	US-08-687-421-1	Sequence 1, Appl
161	28	11.2	2409	3	US-09-293-322C-8	Sequence 8, Appl	c 234	27	10.8	77	4	US-09-412-017-1	Sequence 1, Appl
162	28	11.2	2409	3	US-08-439-497A-8	Sequence 8, Appl	c 235	27	10.8	77	4	US-09-502-344-38	Sequence 38, Appl
163	28	11.2	3083	3	US-08-956-657-1	Sequence 1, Appl	c 236	27	10.8	77	4	US-09-364-539-6	Sequence 6, Appl
164	28	11.2	3083	4	US-09-335-231-25	Sequence 25, Appl	c 237	27	10.8	77	5	PCT-US95-05600-140	Sequence 140, App
165	28	11.2	19806	4	US-09-740-028A-3	Sequence 3, Appl	c 238	27	10.8	77	5	PCT-US95-11982-4	Sequence 4, Appl
166	27	10.8	34	3	US-08-974-549A-531	Sequence 531, App	c 239	27	10.8	77	5	PCT-US96-09537-206	Sequence 206, App
c 167	27	10.8	34	4	US-08-912-951-298	Sequence 298, App	c 240	27	10.8	78	3	US-08-946-138-26	Sequence 26, Appl
c 168	27	10.8	39	1	US-08-575-361A-19	Sequence 19, Appl	c 241	27	10.8	87	1	US-08-199-507B-54	Sequence 54, Appl
c 169	27	10.8	39	1	US-08-575-361A-20	Sequence 20, Appl	c 242	27	10.8	87	1	US-08-243-870-2	Sequence 2, Appl
170	27	10.8	40	3	US-08-974-549A-533	Sequence 533, App	243	27	10.8	87	1	US-08-477-530-1	Sequence 1, Appl
171	27	10.8	40	3	US-09-275-850-348	Sequence 348, App	244	27	10.8	87	1	US-08-477-530-1	Sequence 1, Appl
172	27	10.8	40	4	US-08-912-951-300	Sequence 300, App	245	27	10.8	87	1	US-08-409-439A-2	Sequence 2, Appl
173	27	10.8	46	3	US-08-974-549A-534	Sequence 534, App	246	27	10.8	87	1	US-08-477-830-1	Sequence 1, Appl

C 247	27	10.8	87	1	US-08-433-136A-40	Sequence 40, Appl	320	27	10.8	107	5	PCT-US95-05600-18	Sequence 18, Appl
C 248	27	10.8	87	1	US-08-309-245-2	Sequence 2, Appl	C 321	27	10.8	107	5	PCT-US95-05600-21	Sequence 21, Appl
C 249	27	10.8	87	1	US-08-462-389-2	Sequence 2, Appl	C 322	27	10.8	139	4	US-08-679-493A-60	Sequence 60, Appl
C 250	27	10.8	87	1	US-08-458-423A-49	Sequence 49, Appl	C 323	27	10.8	141	1	US-08-375-116A-131	Sequence 131, Appl
C 251	27	10.8	87	1	US-08-458-423A-52	Sequence 52, Appl	C 324	27	10.8	142	1	US-08-375-116A-130	Sequence 130, Appl
C 252	27	10.8	87	1	US-08-458-424B-49	Sequence 49, Appl	C 325	27	10.8	142	2	US-08-618-700-6	Sequence 6, Appl
C 253	27	10.8	87	1	US-08-458-424B-52	Sequence 54, Appl	C 326	27	10.8	147	2	US-08-618-700-7	Sequence 7, Appl
C 254	27	10.8	87	1	US-08-441-828-54	Sequence 54, Appl	C 327	27	10.8	147	3	US-09-157-601-6	Sequence 6, Appl
C 255	27	10.8	87	1	US-08-433-124A-40	Sequence 12, Appl	C 328	27	10.8	147	3	US-09-157-601-7	Sequence 7, Appl
C 256	27	10.8	87	1	US-08-463-101-2	Sequence 12, Appl	C 329	27	10.8	147	3	US-09-157-601-7	Sequence 7, Appl
C 257	27	10.8	87	1	US-08-591-989-12	Sequence 12, Appl	C 330	27	10.8	147	3	US-09-157-601-7	Sequence 7, Appl
C 258	27	10.8	87	2	US-08-488-402A-64	Sequence 64, Appl	C 331	27	10.8	154	2	US-08-721-684C-7	Sequence 7, Appl
C 259	27	10.8	87	2	US-08-488-402A-79	Sequence 79, Appl	C 332	27	10.8	154	2	US-09-005-970-7	Sequence 7, Appl
C 260	27	10.8	87	2	US-08-484-522A-64	Sequence 64, Appl	C 333	27	10.8	154	3	US-09-407-715-7	Sequence 7, Appl
C 261	27	10.8	87	2	US-08-484-522A-79	Sequence 79, Appl	C 334	27	10.8	208	1	US-08-375-116A-132	Sequence 132, Appl
C 262	27	10.8	87	2	US-08-618-700-2	Sequence 2, Appl	C 335	27	10.8	208	1	US-08-375-116A-132	Sequence 132, Appl
C 263	27	10.8	87	2	US-08-799-949-2	Sequence 2, Appl	C 336	27	10.8	231	4	US-08-679-493A-13	Sequence 13, Appl
C 264	27	10.8	87	2	US-08-777-527A-74	Sequence 74, Appl	C 337	27	10.8	252	4	US-09-313-294A-1788	Sequence 1788, Ap
C 265	27	10.8	87	2	US-08-477-527A-186	Sequence 186, App	C 338	27	10.8	265	4	US-09-313-294A-211	Sequence 211, App
C 266	27	10.8	87	3	US-08-481-710-7A	Sequence 74, Appl	C 339	27	10.8	268	4	US-09-313-294A-1104	Sequence 1104, Ap
C 267	27	10.8	87	3	US-08-481-710-186	Sequence 186, App	C 340	27	10.8	271	4	US-09-313-294A-378	Sequence 378, App
C 268	27	10.8	87	3	US-08-793-398-2	Sequence 2, Appl	C 341	27	10.8	279	4	US-09-313-294A-3409	Sequence 3409, Ap
C 269	27	10.8	87	3	US-08-793-398-4	Sequence 4, Appl	C 342	27	10.8	282	4	US-09-313-294A-2238	Sequence 2238, Ap
C 270	27	10.8	87	3	US-09-157-601-2	Sequence 2, Appl	C 343	27	10.8	282	4	US-09-313-294A-4180	Sequence 4180, Ap
C 271	27	10.8	87	3	US-08-976-413A-40	Sequence 40, Appl	C 344	27	10.8	292	4	US-09-313-294A-811	Sequence 811, App
C 272	27	10.8	87	3	US-08-973-124-49	Sequence 49, Appl	C 345	27	10.8	303	4	US-09-313-294A-5823	Sequence 5823, Ap
C 273	27	10.8	87	3	US-08-973-124-52	Sequence 52, Appl	C 346	27	10.8	305	4	US-09-254-352B-49	Sequence 49, Appl
C 274	27	10.8	87	3	US-09-335-012-44	Sequence 44, Appl	C 347	27	10.8	348	4	US-09-313-294A-5875	Sequence 5875, Ap
C 275	27	10.8	87	4	US-09-364-539-192	Sequence 192, App	C 348	27	10.8	345	4	US-09-025-203-16	Sequence 16, Appl
C 276	27	10.8	87	4	US-09-941-964-44	Sequence 44, Appl	C 349	27	10.8	468	3	US-08-821-994-36	Sequence 36, Appl
C 277	27	10.8	87	4	US-10-096-830-44	Sequence 44, Appl	C 350	27	10.8	493	4	US-09-736-457-13	Sequence 13, Appl
C 278	27	10.8	87	5	PCT-US95-11982-2	Sequence 2, Appl	C 351	27	10.8	493	4	US-09-736-457-13	Sequence 13, Appl
C 279	27	10.8	87	5	PCT-US95-11982A-2	Sequence 2, Appl	C 352	27	10.8	495	2	US-08-465-380-31	Sequence 31, Appl
C 280	27	10.8	87	5	PCT-US95-11982A-4	Sequence 4, Appl	C 353	27	10.8	495	2	US-08-486-397-31	Sequence 31, Appl
C 281	27	10.8	87	5	PCT-US96-06059-40	Sequence 40, Appl	C 354	27	10.8	495	2	US-08-486-399-31	Sequence 31, Appl
C 282	27	10.8	87	5	PCT-US96-08014-49	Sequence 49, Appl	C 355	27	10.8	495	2	US-08-461-965-31	Sequence 31, Appl
C 283	27	10.8	87	5	PCT-US96-08014-52	Sequence 52, Appl	C 356	27	10.8	558	2	US-08-647-368A-3	Sequence 3, Appl
C 284	27	10.8	87	5	PCT-US96-09472-64	Sequence 64, Appl	C 357	27	10.8	750	3	US-08-821-994-40	Sequence 40, Appl
C 285	27	10.8	87	5	PCT-US96-09472-79	Sequence 79, Appl	C 358	27	10.8	763	4	US-09-484-970B-166	Sequence 166, App
C 286	27	10.8	87	5	PCT-US96-09537-74	Sequence 74, Appl	C 359	27	10.8	780	4	US-09-867-915-27	Sequence 27, Appl
C 287	27	10.8	87	5	PCT-US96-09537-186	Sequence 186, App	C 360	27	10.8	808	3	US-08-791-115B-12	Sequence 12, Appl
C 288	27	10.8	90	4	US-09-314-268-177	Sequence 177, App	C 361	27	10.8	808	4	US-09-140-749-23	Sequence 23, Appl
C 289	27	10.8	92	4	US-09-223-139-27	Sequence 27, Appl	C 362	27	10.8	890	4	US-09-016-434-872	Sequence 872, App
C 290	27	10.8	92	4	US-09-223-139-27	Sequence 27, Appl	C 363	27	10.8	897	3	US-09-621-233-1	Sequence 1, Appl
C 291	27	10.8	92	5	PCT-US96-11473A-1	Sequence 1, Appl	C 364	27	10.8	897	4	US-09-724-508-1	Sequence 1, Appl
C 292	27	10.8	92	5	PCT-US96-11473A-1	Sequence 1, Appl	C 365	27	10.8	897	4	US-09-724-516-1	Sequence 1, Appl
C 293	27	10.8	94	4	US-09-364-539-5	Sequence 5, Appl	C 366	27	10.8	1007	4	US-09-328-475C-106	Sequence 106, App
C 294	27	10.8	96	1	US-08-478-783A-36	Sequence 36, Appl	C 367	27	10.8	1024	4	US-09-328-475C-44	Sequence 44, Appl
C 295	27	10.8	96	1	US-08-478-725-36	Sequence 36, Appl	C 368	27	10.8	1024	4	US-09-328-475C-49	Sequence 49, Appl
C 296	27	10.8	96	1	US-08-618-693-36	Sequence 36, Appl	C 369	27	10.8	1024	4	US-09-328-475C-49	Sequence 49, Appl
C 297	27	10.8	96	3	US-08-973-124-125	Sequence 125, App	C 370	27	10.8	1094	4	US-09-280-116-243	Sequence 243, App
C 298	27	10.8	96	3	US-08-991-743C-36	Sequence 36, Appl	C 371	27	10.8	1233	3	US-09-276-531-7	Sequence 7, Appl
C 299	27	10.8	96	5	PCT-US96-08014-125	Sequence 36, Appl	C 372	27	10.8	1461	3	US-08-445-463B-5	Sequence 5, Appl
C 300	27	10.8	96	5	PCT-US96-08014-125	Sequence 125, App	C 373	27	10.8	1461	3	US-08-445-464C-5	Sequence 5, Appl
C 301	27	10.8	97	1	US-08-447-172A-1	Sequence 1, Appl	C 374	27	10.8	1461	4	US-08-044-857D-5	Sequence 5, Appl
C 302	27	10.8	97	1	US-08-447-172A-1	Sequence 1, Appl	C 375	27	10.8	1461	5	PCT-US94-03437-5	Sequence 5, Appl
C 303	27	10.8	97	3	US-08-952-793-348	Sequence 348, App	C 376	27	10.8	1474	4	US-09-508-542-17	Sequence 17, Appl
C 304	27	10.8	97	3	US-08-952-793-390	Sequence 280, App	C 377	27	10.8	1474	4	US-09-508-542-17	Sequence 17, Appl
C 305	27	10.8	97	4	US-09-843-928-248	Sequence 248, App	C 378	27	10.8	1576	5	PCT-US95-11405-34	Sequence 34, Appl
C 306	27	10.8	97	4	US-09-843-928-390	Sequence 390, App	C 379	27	10.8	1608	1	US-07-621-670-2	Sequence 2, Appl
C 307	27	10.8	97	5	PCT-US96-09455A-248	Sequence 248, App	C 380	27	10.8	1738	3	US-09-120-365-89	Sequence 89, Appl
C 308	27	10.8	99	4	US-08-679-493A-18	Sequence 30, Appl	C 381	27	10.8	1738	3	US-09-515-039-89	Sequence 89, Appl
C 309	27	10.8	99	4	US-08-679-493A-18	Sequence 18, Appl	C 382	27	10.8	2030	4	US-09-484-970B-152	Sequence 152, App
C 310	27	10.8	104	2	US-08-591-989-11	Sequence 11, Appl	C 383	27	10.8	2087	4	US-09-484-970B-153	Sequence 153, App
C 311	27	10.8	104	2	US-08-799-949-1	Sequence 1, Appl	C 384	27	10.8	2475	4	US-09-624-693A-20	Sequence 20, Appl
C 312	27	10.8	104	4	US-09-364-543-1	Sequence 1, Appl	C 385	27	10.8	2635	4	US-09-186-276B-57	Sequence 57, Appl
C 313	27	10.8	104	4	US-09-364-543-1	Sequence 1, Appl	C 386	27	10.8	2635	4	US-08-843-445-57	Sequence 57, Appl
C 314	27	10.8	107	1	US-08-441-591-1	Sequence 1, Appl	C 387	27	10.8	2635	4	US-09-186-188B-57	Sequence 57, Appl
C 315	27	10.8	107	1	US-08-441-591-4	Sequence 4, Appl	C 388	27	10.8	3083	3	US-08-956-657-1	Sequence 1, Appl
C 316	27	10.8	107	1	US-08-303-362A-1	Sequence 1, Appl	C 389	27	10.8	3083	4	US-09-335-231-25	Sequence 25, Appl
C 317	27	10.8	107	1	US-08-303-362A-4	Sequence 4, Appl	C 390	27	10.8	3720	1	US-08-074-967-1	Sequence 1, Appl
C 318	27	10.8	107	1	US-08-472-194A-23	Sequence 23, Appl	C 391	27	10.8	3720	2	US-08-553-541B-1	Sequence 1, Appl
C 319	27	10.8	107	4	US-08-849-567A-23	Sequence 23, Appl	C 392	27	10.8	3720	3	US-09-268-202-1	Sequence 1, Appl

C 393	27	10.8	3720	5	PCT-US94-06669-1	Sequence 1, Appli	C 466	26	10.4	65	3	US-08-993-170A-78	Sequence 78, Appl
C 394	27	10.8	3837	4	US-09-724-517-1	Sequence 1, Appli	C 467	26	10.4	65	3	US-08-993-775B-78	Sequence 78, Appl
C 395	27	10.8	3837	4	US-09-641-807A-1	Sequence 1, Appli	C 468	26	10.4	66	1	US-08-748-697A-13	Sequence 13, Appl
C 396	27	10.8	3837	4	US-09-723-096A-1	Sequence 1, Appli	C 469	26	10.4	66	2	US-08-659-453B-1	Sequence 1, Appli
C 397	27	10.8	3952	2	US-08-381-691-16	Sequence 16, Appli	C 470	26	10.4	66	3	US-09-089-853A-1	Sequence 1, Appli
C 398	27	10.8	8285	4	US-09-732-025-3	Sequence 3, Appli	C 471	26	10.4	66	3	US-09-131-009A-1	Sequence 1, Appli
C 399	27	10.8	11528	3	US-08-444-644-18	Sequence 18, Appli	C 472	26	10.4	66	3	US-09-092-226A-1	Sequence 1, Appli
C 400	27	10.8	11528	4	US-08-232-246A-18	Sequence 18, Appli	C 473	26	10.4	66	3	US-08-687-421-320	Sequence 320, Appl
C 401	27	10.8	11827	4	US-09-739-455-3	Sequence 3, Appli	C 474	26	10.4	66	3	US-08-130-862A-1	Sequence 1, Appli
C 402	27	10.8	12127	3	US-08-444-644-32	Sequence 32, Appli	C 475	26	10.4	66	3	US-09-090-809A-1	Sequence 1, Appli
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C 406	27	10.8	17138	3	US-09-813-813-3	Sequence 3, Appli	C 479	26	10.4	67	3	US-07-876-288-14	Sequence 14, Appli
C 407	27	10.8	17138	3	US-09-813-813-3	Sequence 3, Appli	C 480	26	10.4	67	5	PCT-US95-05471-3	Sequence 3, Appli
C 408	27	10.8	17138	4	US-09-920-048-3	Sequence 3, Appli	C 481	26	10.4	68	2	US-08-659-453B-9	Sequence 9, Appli
C 409	27	10.8	17138	4	US-09-920-048-3	Sequence 3, Appli	C 482	26	10.4	68	3	US-09-089-853A-9	Sequence 9, Appli
C 410	27	10.8	19650	4	US-09-819-989-3	Sequence 3, Appli	C 483	26	10.4	68	3	US-09-131-003A-9	Sequence 9, Appli
C 411	27	10.8	19650	4	US-09-819-989-3	Sequence 3, Appli	C 484	26	10.4	68	3	US-09-092-226A-9	Sequence 9, Appli
C 412	27	10.8	21784	4	US-09-820-002-3	Sequence 3, Appli	C 485	26	10.4	68	3	US-09-130-862A-9	Sequence 9, Appli
C 413	27	10.8	36159	4	US-09-749-588-3	Sequence 3, Appli	C 486	26	10.4	68	3	US-09-090-809A-9	Sequence 9, Appli
C 414	27	10.8	36159	4	US-09-749-588-3	Sequence 3, Appli	C 487	26	10.4	68	4	US-09-053-116A-9	Sequence 9, Appli
C 415	27	10.8	36551	4	US-09-738-894A-3	Sequence 3, Appli	C 488	26	10.4	70	1	US-08-434-001-71	Sequence 71, Appl
C 416	27	10.8	36551	4	US-09-964-469-3	Sequence 3, Appli	C 489	26	10.4	70	1	US-08-433-585-71	Sequence 71, Appl
C 417	27	10.8	38564	4	US-09-734-673-3	Sequence 3, Appli	C 490	26	10.4	70	1	US-08-437-667-71	Sequence 71, Appl
C 418	27	10.8	46718	4	US-09-816-093-3	Sequence 3, Appli	C 491	26	10.4	70	2	US-08-437-667-71	Sequence 71, Appl
C 419	27	10.8	63588	4	US-09-803-404-3	Sequence 3, Appli	C 492	26	10.4	70	3	US-08-906-955-71	Sequence 71, Appl
C 420	27	10.8	64467	4	US-09-873-671B-3	Sequence 3, Appli	C 493	26	10.4	70	3	US-08-945-909-71	Sequence 71, Appl
C 421	27	10.8	83450	4	US-09-811-469-3	Sequence 3, Appli	C 494	26	10.4	70	4	US-09-396-002A-71	Sequence 71, Appl
C 422	27	10.8	111282	4	US-09-754-250-3	Sequence 3, Appli	C 495	26	10.4	70	5	PCT-US96-06060-71	Sequence 71, Appl
C 423	27	10.8	148567	4	US-09-801-876B-3	Sequence 3, Appli	C 496	26	10.4	71	1	US-08-458-423A-5	Sequence 5, Appli
C 424	27	10.8	174493	4	US-09-804-471A-3	Sequence 3, Appli	C 497	26	10.4	71	1	US-08-458-424B-5	Sequence 5, Appli
C 425	27	10.8	202001	4	US-09-734-674-3	Sequence 3, Appli	C 498	26	10.4	71	3	US-08-973-124-5	Sequence 5, Appli
C 426	27	10.8	202001	4	US-09-734-674-3	Sequence 3, Appli	C 499	26	10.4	71	5	PCT-US96-08014-5	Sequence 5, Appli
C 427	26	10.4	39	2	US-08-659-453B-2	Sequence 2, Appli	C 500	26	10.4	72	3	US-09-115-446-4	Sequence 4, Appli
C 428	26	10.4	39	3	US-09-089-853A-2	Sequence 2, Appli	C 501	26	10.4	73	4	US-09-301-511A-63	Sequence 63, Appl
C 429	26	10.4	39	3	US-09-131-009A-2	Sequence 2, Appli	C 502	26	10.4	73	4	US-09-301-511A-67	Sequence 67, Appl
C 430	26	10.4	39	3	US-09-092-226A-2	Sequence 2, Appli	C 503	26	10.4	73	4	US-09-474-432B-1517	Sequence 1517, Ap
C 431	26	10.4	39	3	US-09-130-862A-2	Sequence 2, Appli	C 504	26	10.4	73	4	US-09-474-432B-1520	Sequence 1520, Ap
C 432	26	10.4	39	3	US-09-275-850-340	Sequence 340, App	C 505	26	10.4	74	3	US-09-193-068-15	Sequence 15, Appl
C 433	26	10.4	39	3	US-09-090-809A-2	Sequence 2, Appli	C 506	26	10.4	75	1	US-08-219-013-27	Sequence 27, Appl
C 434	26	10.4	39	4	US-09-053-116A-2	Sequence 2, Appli	C 507	26	10.4	75	1	US-08-437-815-10	Sequence 10, Appl
C 435	26	10.4	42	2	US-08-659-453B-14	Sequence 14, Appl	C 508	26	10.4	75	3	US-08-897-040-10	Sequence 10, Appl
C 436	26	10.4	42	3	US-09-089-853A-14	Sequence 14, Appl	C 509	26	10.4	75	3	US-08-687-421-215	Sequence 215, App
C 437	26	10.4	42	3	US-09-131-009A-14	Sequence 14, Appl	C 510	26	10.4	76	1	US-08-198-670A-33	Sequence 33, Appl
C 438	26	10.4	42	3	US-09-092-226A-14	Sequence 14, Appl	C 511	26	10.4	76	5	PCT-US95-05600-1	Sequence 1, Appli
C 439	26	10.4	42	3	US-09-130-862A-14	Sequence 14, Appl	C 512	26	10.4	78	1	US-08-484-557C-1	Sequence 1, Appli
C 440	26	10.4	42	3	US-09-053-116A-14	Sequence 14, Appl	C 513	26	10.4	78	2	US-08-487-720A-1	Sequence 1, Appli
C 441	26	10.4	42	3	US-09-090-809A-14	Sequence 14, Appl	C 514	26	10.4	78	3	US-08-945-734-1	Sequence 1, Appli
C 442	26	10.4	44	2	US-08-659-453B-22	Sequence 22, Appl	C 515	26	10.4	78	3	US-09-258-797-1	Sequence 1, Appli
C 443	26	10.4	44	3	US-09-089-853A-22	Sequence 22, Appl	C 516	26	10.4	78	3	US-09-193-068-17	Sequence 17, Appl
C 444	26	10.4	44	3	US-09-131-009A-22	Sequence 22, Appl	C 517	26	10.4	78	5	PCT-US96-09451-1	Sequence 1, Appli
C 445	26	10.4	44	3	US-09-092-226A-22	Sequence 22, Appl	C 518	26	10.4	79	1	US-08-384-708A-4	Sequence 4, Appli
C 446	26	10.4	44	3	US-09-130-862A-22	Sequence 22, Appl	C 519	26	10.4	79	3	US-08-687-421-4	Sequence 4, Appli
C 447	26	10.4	44	4	US-09-090-809A-22	Sequence 22, Appl	C 520	26	10.4	79	3	US-08-471-985A-112	Sequence 112, App
C 448	26	10.4	44	4	US-09-053-116A-22	Sequence 22, Appl	C 521	26	10.4	80	1	US-08-471-985A-112	Sequence 112, App
C 449	26	10.4	46	4	US-09-301-721A-1	Sequence 1, Appli	C 522	26	10.4	80	1	US-08-472-255A-126	Sequence 126, App
C 450	26	10.4	46	4	US-09-301-721A-2	Sequence 2, Appli	C 523	26	10.4	80	1	US-08-472-255A-126	Sequence 126, App
C 451	26	10.4	54	4	US-09-504-132-9	Sequence 9, Appli	C 524	26	10.4	80	1	US-08-472-255A-126	Sequence 126, App
C 452	26	10.4	59	1	US-07-964-624D-13	Sequence 13, Appli	C 525	26	10.4	80	1	US-08-479-724A-126	Sequence 126, App
C 453	26	10.4	59	1	US-08-442-062-13	Sequence 13, Appli	C 526	26	10.4	80	1	US-08-479-724A-126	Sequence 126, App
C 454	26	10.4	60	4	US-08-679-493A-19	Sequence 19, Appli	C 527	26	10.4	80	3	US-08-472-194A-4	Sequence 4, Appli
C 455	26	10.4	61	4	US-08-679-493A-19	Sequence 19, Appli	C 528	26	10.4	80	3	US-08-472-256B-126	Sequence 126, App
C 456	26	10.4	62	2	US-08-659-453B-4	Sequence 4, Appli	C 529	26	10.4	80	3	US-08-472-256B-126	Sequence 126, App
C 457	26	10.4	62	3	US-09-089-853A-4	Sequence 4, Appli	C 530	26	10.4	80	3	US-09-193-068-23	Sequence 23, Appl
C 458	26	10.4	62	3	US-09-131-009A-4	Sequence 4, Appli	C 531	26	10.4	80	3	US-08-952-793-126	Sequence 126, App
C 459	26	10.4	62	3	US-09-092-226A-4	Sequence 4, Appli	C 532	26	10.4	80	3	US-08-952-793-126	Sequence 126, App
C 460	26	10.4	62	3	US-09-130-862A-4	Sequence 4, Appli	C 533	26	10.4	80	4	US-08-849-567A-4	Sequence 4, Appli
C 461	26	10.4	62	3	US-09-090-809A-4	Sequence 4, Appli	C 534	26	10.4	80	4	US-09-849-928-126	Sequence 126, App
C 462	26	10.4	62	3	US-09-053-116A-4	Sequence 4, Appli	C 535	26	10.4	80	4	US-09-849-928-126	Sequence 126, App
C 463	26	10.4	63	4	US-08-973-131-22	Sequence 22, Appl	C 536	26	10.4	80	5	PCT-US95-12401A-112	Sequence 112, App
C 464	26	10.4	65	3	US-08-996-441B-78	Sequence 78, Appl	C 537	26	10.4	80	5	PCT-US95-12401A-112	Sequence 112, App
C 465	26	10.4	65	3	US-08-993-722A-78	Sequence 78, Appl	C 538	26	10.4	80	5	PCT-US96-09455A-126	Sequence 126, App

c 539	26	10.4	80	5	PCT-US96-09455A-126	Sequence 126, App	612	26	10.4	142	1	US-08-375-116A-130	Sequence 130, App
540	26	10.4	81	1	US-08-447-169A-240	Sequence 240, App	c 613	26	10.4	149	3	US-08-903-139B-31	Sequence 31, Appl
c 541	26	10.4	81	1	US-08-447-169A-240	Sequence 240, App	614	26	10.4	150	3	US-08-139-176D-1	Sequence 1, Appli
542	26	10.4	82	4	US-08-679-493A-14	Sequence 14, Appl	615	26	10.4	150	3	US-09-041-841-1	Sequence 1, Appli
543	26	10.4	82	4	US-08-363-939A-9	Sequence 9, Appli	c 616	26	10.4	152	2	US-08-771-201-8	Sequence 8, Appli
c 544	26	10.4	82	4	US-08-363-939A-9	Sequence 9, Appli	c 617	26	10.4	155	3	US-08-903-139B-15	Sequence 15, Appl
545	26	10.4	83	3	US-08-687-421-325	Sequence 325, App	618	26	10.4	177	1	US-08-244-116B-18	Sequence 18, Appl
c 546	26	10.4	85	3	US-09-275-850-338	Sequence 338, App	619	26	10.4	184	4	US-09-313-294A-6933	Sequence 6933, Ap
547	26	10.4	85	3	US-09-275-850-339	Sequence 339, App	620	26	10.4	185	4	US-09-186-276B-64	Sequence 64, Appl
c 548	26	10.4	86	1	US-07-964-624D-43	Sequence 43, Appl	621	26	10.4	195	4	US-08-842-445-64	Sequence 64, Appl
549	26	10.4	86	1	US-08-442-062-43	Sequence 43, Appl	622	26	10.4	195	4	US-08-186-188B-64	Sequence 64, Appl
c 550	26	10.4	86	1	US-08-748-597A-43	Sequence 43, Appl	c 623	26	10.4	199	4	US-09-186-276B-60	Sequence 60, Appl
551	26	10.4	86	4	US-09-165-616-43	Sequence 43, Appl	c 624	26	10.4	199	4	US-08-842-445-60	Sequence 60, Appl
c 552	26	10.4	88	4	US-09-363-939A-5	Sequence 5, Appli	c 625	26	10.4	199	4	US-09-186-188B-60	Sequence 60, Appl
c 553	26	10.4	88	4	US-09-363-939A-5	Sequence 5, Appli	626	26	10.4	202	2	US-08-039-198B-6	Sequence 6, Appli
c 554	26	10.4	90	4	US-08-679-493A-17	Sequence 17, Appl	c 627	26	10.4	215	4	US-09-313-294A-6241	Sequence 6241, Ap
c 555	26	10.4	92	4	US-09-301-511A-62	Sequence 62, Appl	628	26	10.4	231	4	US-08-679-493A-13	Sequence 13, Appl
556	26	10.4	93	1	US-08-458-423A-2	Sequence 2, Appli	629	26	10.4	242	4	US-09-313-294A-4646	Sequence 4646, Ap
c 557	26	10.4	93	1	US-08-458-424B-2	Sequence 2, Appli	630	26	10.4	242	4	US-09-016-434-478	Sequence 478, App
c 558	26	10.4	93	3	US-08-973-124-2	Sequence 2, Appli	c 631	26	10.4	244	4	US-09-016-434-478	Sequence 478, App
559	26	10.4	93	4	US-09-474-432B-1524	Sequence 1524, Ap	c 632	26	10.4	244	4	US-09-016-434-478	Sequence 478, App
c 560	26	10.4	93	5	PCT-US96-08014-2	Sequence 2, Appli	c 633	26	10.4	259	3	US-09-103-359-13	Sequence 13, Appl
561	26	10.4	95	1	US-08-458-423A-4	Sequence 4, Appli	c 634	26	10.4	265	4	US-09-313-294A-211	Sequence 211, App
562	26	10.4	95	1	US-08-458-424B-4	Sequence 4, Appli	635	26	10.4	265	4	US-09-313-294A-1611	Sequence 1611, Ap
563	26	10.4	95	3	US-08-973-124-4	Sequence 4, Appli	636	26	10.4	267	4	US-09-107-532A-3091	Sequence 3091, Ap
564	26	10.4	95	5	PCT-US96-08014-4	Sequence 4, Appli	637	26	10.4	268	4	US-09-313-294A-1758	Sequence 1758, Ap
565	26	10.4	96	1	US-08-234-613-1	Sequence 1, Appli	638	26	10.4	269	4	US-09-313-294A-6033	Sequence 6033, Ap
566	26	10.4	96	1	US-08-753-054-19	Sequence 19, Appl	639	26	10.4	270	4	US-09-313-294A-3632	Sequence 3632, Ap
c 567	26	10.4	96	2	US-08-237-973-1	Sequence 1, Appli	c 640	26	10.4	272	4	US-09-313-294A-435	Sequence 435, App
c 568	26	10.4	98	1	US-08-399-412A-7	Sequence 7, Appli	c 641	26	10.4	275	4	US-09-313-294A-1943	Sequence 1943, Ap
c 569	26	10.4	98	1	US-08-447-172A-28	Sequence 28, Appl	642	26	10.4	277	4	US-09-313-294A-2692	Sequence 2692, Ap
c 570	26	10.4	98	1	US-08-447-172A-31	Sequence 31, Appl	c 643	26	10.4	278	4	US-09-313-294A-4472	Sequence 4472, Ap
c 571	26	10.4	98	1	US-08-472-255A-1	Sequence 1, Appli	c 644	26	10.4	278	4	US-09-313-294A-4547	Sequence 4547, Ap
c 572	26	10.4	98	1	US-08-472-256B-1	Sequence 1, Appli	645	26	10.4	279	4	US-09-313-294A-100	Sequence 100, App
c 573	26	10.4	98	3	US-08-952-793-1	Sequence 1, Appli	c 646	26	10.4	279	4	US-09-313-294A-3975	Sequence 3975, Ap
c 574	26	10.4	98	3	US-08-952-793-1	Sequence 1, Appli	c 647	26	10.4	282	4	US-09-313-294A-6434	Sequence 6434, Ap
c 575	26	10.4	98	4	US-08-849-567A-50	Sequence 50, Appl	648	26	10.4	285	4	US-09-107-532A-3089	Sequence 3089, Ap
c 576	26	10.4	98	4	US-08-849-567A-50	Sequence 50, Appl	649	26	10.4	285	4	US-09-313-294A-6745	Sequence 6745, Ap
c 577	26	10.4	98	5	PCT-US96-09455A-1	Sequence 1, Appli	c 650	26	10.4	286	4	US-09-313-294A-3984	Sequence 3984, Ap
c 578	26	10.4	99	4	US-08-679-493A-18	Sequence 18, Appl	c 651	26	10.4	287	4	US-09-313-294A-6402	Sequence 6402, Ap
c 579	26	10.4	99	4	US-08-849-567A-51	Sequence 51, Appl	c 652	26	10.4	288	4	US-09-313-294A-4782	Sequence 4782, Ap
c 580	26	10.4	100	1	US-08-198-670A-37	Sequence 2, Appli	c 653	26	10.4	290	4	US-09-313-294A-6567	Sequence 6567, Ap
c 581	26	10.4	100	5	PCT-US93-09695-2	Sequence 2, Appli	c 654	26	10.4	290	4	US-09-313-294A-6647	Sequence 6647, Ap
c 582	26	10.4	101	1	US-07-843-125-6	Sequence 6, Appli	c 655	26	10.4	291	4	US-09-313-294A-6845	Sequence 6845, Ap
c 583	26	10.4	104	1	US-08-198-670A-36	Sequence 36, Appl	656	26	10.4	292	4	US-09-313-294A-5439	Sequence 5439, Ap
584	26	10.4	104	1	US-08-198-670A-37	Sequence 37, Appl	c 657	26	10.4	292	4	US-09-313-294A-6396	Sequence 6396, Ap
c 585	26	10.4	104	2	US-08-139-176D-2	Sequence 2, Appli	c 658	26	10.4	293	4	US-09-313-294A-6217	Sequence 6217, Ap
586	26	10.4	104	2	US-08-139-176D-3	Sequence 3, Appli	659	26	10.4	293	4	US-09-313-294A-6465	Sequence 6465, Ap
587	26	10.4	104	3	US-09-041-841-2	Sequence 2, Appli	660	26	10.4	294	4	US-09-313-294A-4086	Sequence 4086, Ap
c 588	26	10.4	105	1	US-08-215-012-52	Sequence 52, Appli	c 661	26	10.4	295	4	US-09-313-294A-5741	Sequence 5741, Ap
c 589	26	10.4	105	3	US-08-687-421-240	Sequence 240, App	662	26	10.4	295	4	US-09-313-294A-4086	Sequence 4086, Ap
c 590	26	10.4	106	1	US-07-843-125-8	Sequence 8, Appli	663	26	10.4	296	4	US-09-313-294A-4620	Sequence 4620, Ap
c 591	26	10.4	107	1	US-08-472-194A-23	Sequence 23, Appl	c 664	26	10.4	297	4	US-09-313-294A-6271	Sequence 6271, Ap
c 592	26	10.4	107	3	US-08-193-068-21	Sequence 21, Appl	c 665	26	10.4	298	4	US-09-313-294A-5861	Sequence 5861, Ap
593	26	10.4	107	3	US-08-845-567A-23	Sequence 23, Appl	c 666	26	10.4	300	4	US-09-313-294A-7389	Sequence 7389, Ap
c 594	26	10.4	108	4	US-08-296-328A-15	Sequence 15, Appl	667	26	10.4	301	4	US-09-313-294A-4954	Sequence 4954, Ap
c 595	26	10.4	108	4	US-08-299-498A-3	Sequence 3, Appli	c 668	26	10.4	304	4	US-09-313-294A-7085	Sequence 7085, Ap
c 596	26	10.4	110	1	PCT-US95-10813-3	Sequence 3, Appli	669	26	10.4	305	4	US-09-254-352B-49	Sequence 49, Appl
c 597	26	10.4	110	5	US-08-299-498A-32	Sequence 32, Appl	c 670	26	10.4	305	4	US-09-313-294A-5875	Sequence 5875, Ap
c 598	26	10.4	112	1	US-08-299-498A-32	Sequence 32, Appl	671	26	10.4	315	1	US-07-903-466-41	Sequence 41, Appl
c 599	26	10.4	112	5	PCT-US95-10813-32	Sequence 32, Appl	c 672	26	10.4	315	1	US-07-903-466-41	Sequence 41, Appl
600	26	10.4	117	1	US-08-458-423A-1	Sequence 1, Appli	673	26	10.4	315	5	PCT-US93-05794-41	Sequence 41, Appl
601	26	10.4	117	1	US-08-458-424B-1	Sequence 1, Appli	c 674	26	10.4	315	5	PCT-US93-05794-41	Sequence 41, Appl
602	26	10.4	117	3	US-08-973-124-1	Sequence 1, Appli	675	26	10.4	319	4	US-09-313-294A-5074	Sequence 5074, Ap
603	26	10.4	117	5	PCT-US96-08014-1	Sequence 1, Appli	676	26	10.4	324	2	US-08-378-939-21	Sequence 21, Appl
c 604	26	10.4	119	4	US-08-679-493A-15	Sequence 15, Appl	c 677	26	10.4	324	2	US-08-378-939-27	Sequence 27, Appl
c 605	26	10.4	122	3	US-09-193-068-16	Sequence 16, Appl	678	26	10.4	345	4	US-09-025-203-16	Sequence 16, Appl
c 606	26	10.4	122	3	US-09-193-068-16	Sequence 16, Appl	c 679	26	10.4	348	4	US-09-672-609-18	Sequence 18, Appl
c 607	26	10.4	132	2	US-08-771-201-7	Sequence 7, Appli	c 680	26	10.4	348	4	US-09-025-403A-18	Sequence 18, Appl
c 608	26	10.4	134	1	US-08-299-498A-5	Sequence 5, Appli	681	26	10.4	369	4	US-09-107-532A-3090	Sequence 3090, Ap
609	26	10.4	134	5	PCT-US95-10813-5	Sequence 5, Appli	682	26	10.4	414	4	US-09-107-532A-3054	Sequence 3054, Ap
610	26	10.4	137	4	US-09-466-994-2	Sequence 2, Appli	683	26	10.4	416	4	US-08-484-841A-13	Sequence 13, Appl
611	26	10.4	137	4	US-08-679-493A-60	Sequence 60, Appl	c 684	26	10.4	423	2	US-08-822-028-62	Sequence 62, Appl

C 685	26	10.4	423	3	US-08-479-285-62	Sequence 62, Appl	C 758	26	10.4	2379	4	US-09-484-970B-139	Sequence 139, Appl
C 686	26	10.4	451	4	US-09-582-200A-9	Sequence 9, Appl	C 759	26	10.4	2428	2	US-08-849-536A-3	Sequence 3, Appl
C 687	26	10.4	432	4	US-09-582-200A-8	Sequence 8, Appl	C 760	26	10.4	2793	1	US-08-209-747-1	Sequence 1, Appl
C 688	26	10.4	479	4	US-09-254-352B-39	Sequence 39, Appl	C 761	26	10.4	2793	1	US-08-458-298-1	Sequence 22, Appl
C 689	26	10.4	555	3	US-09-109-205-8	Sequence 8, Appl	C 762	26	10.4	2847	4	US-09-484-970B-22	Sequence 22, Appl
C 690	26	10.4	555	4	US-09-495-050A-96	Sequence 96, Appl	C 763	26	10.4	3350	4	US-09-894-998A-48	Sequence 48, Appl
C 691	26	10.4	563	3	US-09-276-531-38	Sequence 38, Appl	C 764	26	10.4	3450	4	US-09-462-561B-10	Sequence 10, Appl
C 692	26	10.4	595	3	US-09-276-531-63	Sequence 63, Appl	C 765	26	10.4	3556	3	US-09-276-531-8	Sequence 8, Appl
C 693	26	10.4	595	3	US-09-276-531-63	Sequence 63, Appl	C 766	26	10.4	3556	3	US-08-845-161A-5	Sequence 5, Appl
C 694	26	10.4	602	4	US-09-334-818A-15	Sequence 15, Appl	C 767	26	10.4	3846	2	US-08-845-161A-5	Sequence 5, Appl
C 695	26	10.4	605	3	US-09-109-204-19	Sequence 19, Appl	C 768	26	10.4	3846	3	US-09-270-751-5	Sequence 5, Appl
C 696	26	10.4	605	3	US-09-109-204-19	Sequence 19, Appl	C 769	26	10.4	3846	3	US-09-270-751-5	Sequence 5, Appl
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C 698	26	10.4	605	4	US-09-490-032-19	Sequence 19, Appl	C 771	26	10.4	3846	4	US-09-168-218B-3	Sequence 3, Appl
C 699	26	10.4	608	1	US-08-386-495-11	Sequence 11, Appl	C 772	26	10.4	3900	4	US-09-484-970B-27	Sequence 27, Appl
C 700	26	10.4	608	5	PCT-US96-02331-11	Sequence 11, Appl	C 773	26	10.4	3915	2	US-08-485-139-6	Sequence 6, Appl
C 701	26	10.4	616	3	US-09-276-531-39	Sequence 39, Appl	C 774	26	10.4	3915	3	US-08-750-357-6	Sequence 6, Appl
C 702	26	10.4	633	4	US-09-812-484-25	Sequence 25, Appl	C 775	26	10.4	4339	4	US-09-484-970B-164	Sequence 164, Appl
C 703	26	10.4	633	4	US-09-812-484-25	Sequence 25, Appl	C 776	26	10.4	4339	4	US-08-651-472-64	Sequence 64, Appl
C 704	26	10.4	729	6	5182210-21	Patent No. 5182210	C 777	26	10.4	4701	3	US-08-358-928-64	Sequence 64, Appl
C 705	26	10.4	759	3	US-09-109-205-11	Sequence 11, Appl	C 778	26	10.4	4772	4	US-09-484-970B-133	Sequence 133, Appl
C 706	26	10.4	763	4	US-09-484-970B-166	Sequence 166, Appl	C 779	26	10.4	4858	4	US-09-392-184-1	Sequence 1, Appl
C 707	26	10.4	789	4	US-09-495-050A-8	Sequence 8, Appl	C 780	26	10.4	4858	4	US-09-392-184-1	Sequence 1, Appl
C 708	26	10.4	804	3	US-09-276-531-54	Sequence 54, Appl	C 781	26	10.4	4997	1	US-08-232-463-1	Sequence 6, Appl
C 709	26	10.4	830	3	US-08-387-707-13	Sequence 13, Appl	C 782	26	10.4	5904	2	US-08-311-363-6	Sequence 6, Appl
C 710	26	10.4	830	3	US-08-387-707-13	Sequence 13, Appl	C 783	26	10.4	6045	4	US-09-091-501B-7	Sequence 7, Appl
C 711	26	10.4	830	4	US-08-405-271A-13	Sequence 13, Appl	C 784	26	10.4	6775	4	US-08-462-014-2	Sequence 2, Appl
C 712	26	10.4	830	4	US-08-405-271A-13	Sequence 13, Appl	C 785	26	10.4	8299	1	US-08-462-014-2	Sequence 2, Appl
C 713	26	10.4	869	2	US-08-760-745-2	Sequence 2, Appl	C 786	26	10.4	8299	3	US-08-923-137-3	Sequence 3, Appl
C 714	26	10.4	887	3	US-09-276-531-4	Sequence 4, Appl	C 787	26	10.4	8299	3	US-08-923-137-3	Sequence 3, Appl
C 715	26	10.4	897	3	US-09-276-531-4	Sequence 4, Appl	C 788	26	10.4	8299	3	US-08-973-334-5	Sequence 5, Appl
C 716	26	10.4	915	4	US-09-107-532A-3508	Sequence 3508, Appl	C 789	26	10.4	8313	1	US-08-232-463-2	Sequence 2, Appl
C 717	26	10.4	959	4	US-09-724-510-1	Sequence 1, Appl	C 790	26	10.4	8575	5	PCT-US92-08258-6	Sequence 6, Appl
C 718	26	10.4	959	4	US-09-723-216-1	Sequence 1, Appl	C 791	26	10.4	8575	5	PCT-US92-08258-6	Sequence 6, Appl
C 719	26	10.4	959	4	US-09-675-227-1	Sequence 1, Appl	C 792	26	10.4	8775	1	US-08-232-463-5	Sequence 5, Appl
C 720	26	10.4	960	1	US-08-624-125-13	Sequence 13, Appl	C 793	26	10.4	8775	1	US-08-232-463-5	Sequence 5, Appl
C 721	26	10.4	960	1	US-08-624-125-13	Sequence 13, Appl	C 794	26	10.4	9454	1	US-08-232-463-3	Sequence 3, Appl
C 722	26	10.4	960	4	US-08-937-155-13	Sequence 13, Appl	C 795	26	10.4	9454	1	US-08-232-463-3	Sequence 3, Appl
C 723	26	10.4	960	4	US-08-937-155-13	Sequence 13, Appl	C 796	26	10.4	10249	4	US-09-186-002-14	Sequence 14, Appl
C 724	26	10.4	1001	4	US-09-371-317-142	Sequence 142, Appl	C 797	26	10.4	10249	4	US-09-186-002-14	Sequence 14, Appl
C 725	26	10.4	1070	4	US-09-718-810-3	Sequence 3, Appl	C 798	26	10.4	10320	4	US-09-091-501B-9	Sequence 9, Appl
C 726	26	10.4	1070	4	US-09-718-810-3	Sequence 3, Appl	C 799	26	10.4	10339	4	US-09-186-002-13	Sequence 13, Appl
C 727	26	10.4	1083	3	US-09-276-531-30	Sequence 30, Appl	C 800	26	10.4	10785	3	US-08-444-644-27	Sequence 27, Appl
C 728	26	10.4	1143	3	US-09-276-531-103	Sequence 103, Appl	C 801	26	10.4	10785	3	US-08-444-644-27	Sequence 27, Appl
C 729	26	10.4	1171	4	US-09-636-382A-14	Sequence 14, Appl	C 802	26	10.4	10785	4	US-08-232-246A-27	Sequence 27, Appl
C 730	26	10.4	1171	4	US-09-636-382A-14	Sequence 14, Appl	C 803	26	10.4	10785	4	US-08-232-246A-27	Sequence 27, Appl
C 731	26	10.4	1183	2	US-08-731-722-8	Sequence 8, Appl	C 804	26	10.4	10844	3	US-08-444-644-41	Sequence 41, Appl
C 732	26	10.4	1238	3	US-09-313-300-10	Sequence 10, Appl	C 805	26	10.4	10844	3	US-08-444-644-41	Sequence 41, Appl
C 733	26	10.4	1252	3	US-09-276-531-92	Sequence 92, Appl	C 806	26	10.4	10844	4	US-08-232-246A-41	Sequence 41, Appl
C 734	26	10.4	1457	2	US-08-039-198B-8	Sequence 8, Appl	C 807	26	10.4	11528	3	US-08-232-246A-18	Sequence 18, Appl
C 735	26	10.4	1471	2	US-08-039-198B-8	Sequence 8, Appl	C 808	26	10.4	11528	3	US-08-232-246A-18	Sequence 18, Appl
C 736	26	10.4	1474	4	US-09-508-542-17	Sequence 17, Appl	C 809	26	10.4	12127	3	US-08-444-644-32	Sequence 32, Appl
C 737	26	10.4	1474	4	US-09-508-542-17	Sequence 17, Appl	C 810	26	10.4	12127	3	US-08-444-644-32	Sequence 32, Appl
C 738	26	10.4	1495	4	US-09-364-230-11	Sequence 11, Appl	C 811	26	10.4	12127	4	US-08-232-246A-32	Sequence 32, Appl
C 739	26	10.4	1576	5	PCT-US95-11405-34	Sequence 34, Appl	C 812	26	10.4	15788	4	US-09-484-970B-60	Sequence 60, Appl
C 740	26	10.4	1651	4	US-09-484-970B-17	Sequence 17, Appl	C 813	26	10.4	15788	4	US-09-920-759-13	Sequence 13, Appl
C 741	26	10.4	1689	4	US-09-718-841-1	Sequence 1, Appl	C 814	26	10.4	18853	4	US-09-820-005-3	Sequence 3, Appl
C 742	26	10.4	1689	4	US-09-718-841-1	Sequence 1, Appl	C 815	26	10.4	18853	4	US-09-820-005-3	Sequence 3, Appl
C 743	26	10.4	1721	3	US-08-957-213-2	Sequence 2, Appl	C 816	26	10.4	21784	4	US-09-819-993-3	Sequence 3, Appl
C 744	26	10.4	1769	4	US-09-484-970B-46	Sequence 46, Appl	C 817	26	10.4	28001	4	US-09-819-993-3	Sequence 3, Appl
C 745	26	10.4	1769	4	US-09-484-970B-46	Sequence 46, Appl	C 818	26	10.4	31208	4	US-09-852-067-3	Sequence 3, Appl
C 746	26	10.4	1775	2	US-07-862-588B-5	Sequence 5, Appl	C 819	26	10.4	36651	4	US-09-738-894A-3	Sequence 3, Appl
C 747	26	10.4	2030	4	US-09-484-970B-152	Sequence 152, Appl	C 820	26	10.4	36651	4	US-09-964-469-3	Sequence 3, Appl
C 748	26	10.4	2038	3	US-09-276-531-37	Sequence 37, Appl	C 821	26	10.4	38564	4	US-09-734-673-3	Sequence 3, Appl
C 749	26	10.4	2116	2	US-08-663-566A-18	Sequence 18, Appl	C 822	26	10.4	38564	4	US-09-734-673-3	Sequence 3, Appl
C 750	26	10.4	2116	2	US-08-663-566A-18	Sequence 18, Appl	C 823	26	10.4	62804	4	US-09-800-960-3	Sequence 3, Appl
C 751	26	10.4	2116	2	US-08-023-610-18	Sequence 18, Appl	C 824	26	10.4	63588	4	US-09-873-404-3	Sequence 3, Appl
C 752	26	10.4	2116	2	US-08-362-240A-18	Sequence 18, Appl	C 825	26	10.4	64667	4	US-09-803-671B-3	Sequence 3, Appl
C 753	26	10.4	2215	5	PCT-US95-10245-18	Sequence 18, Appl	C 826	26	10.4	65042	4	US-09-784-316-3	Sequence 3, Appl
C 754	26	10.4	2215	5	PCT-US95-10245-18	Sequence 18, Appl	C 827	26	10.4	74962	4	US-09-685-853A-3	Sequence 3, Appl
C 755	26	10.4	2300	3	US-08-891-789B-7	Sequence 7, Appl	C 828	26	10.4	74962	4	US-09-685-853A-3	Sequence 3, Appl
C 756	26	10.4	2315	1	US-08-103-998-3	Sequence 3, Appl	C 829	26	10.4	75395	4	US-09-984-890-3	Sequence 3, Appl
C 757	26	10.4	2379	4	US-09-484-970B-139	Sequence 139, Appl	C 830	26	10.4	83450	4	US-09-811-469-3	Sequence 3, Appl

C 831	26	10.4	84495	4	US-09-797-906-3	Sequence 3, Appli	C 904	25	10.0	39	4	US-09-053-116A-2	Sequence 2, Appli
C 832	26	10.4	111282	4	US-09-754-250-3	Sequence 3, Appli	C 905	25	10.0	40	3	US-09-028-128A-1	Sequence 1, Appli
C 833	26	10.4	112132	4	US-09-741-150-3	Sequence 3, Appli	C 906	25	10.0	40	3	US-09-028-128A-1	Sequence 1, Appli
C 834	26	10.4	112132	4	US-09-741-150-3	Sequence 3, Appli	C 907	25	10.0	40	3	US-08-974-549A-533	Sequence 533, App
C 835	26	10.4	116592	4	US-09-818-512-3	Sequence 3, Appli	C 908	25	10.0	40	3	US-09-275-850-45	Sequence 45, Appl
C 836	26	10.4	148567	4	US-09-801-876B-3	Sequence 3, Appli	C 909	25	10.0	40	3	US-09-275-850-45	Sequence 45, Appl
C 837	25	10.0	25	3	US-08-779-355-20	Sequence 20, Appl	C 910	25	10.0	40	3	US-09-275-850-348	Sequence 348, App
C 838	25	10.0	25	3	US-08-779-355-20	Sequence 20, Appl	C 911	25	10.0	40	3	US-08-912-951-300	Sequence 300, App
C 839	25	10.0	25	3	US-08-892-747-8	Sequence 8, Appli	C 912	25	10.0	41	2	US-09-004-192A-9	Sequence 9, Appli
C 840	25	10.0	25	3	US-08-892-747-8	Sequence 8, Appli	C 913	25	10.0	41	2	US-09-004-192A-9	Sequence 9, Appli
C 841	25	10.0	25	3	US-08-938-835A-20	Sequence 20, Appl	C 914	25	10.0	42	2	US-08-659-453B-14	Sequence 14, Appl
C 842	25	10.0	25	3	US-08-938-835A-20	Sequence 20, Appl	C 915	25	10.0	42	2	US-09-089-853A-14	Sequence 14, Appl
C 843	25	10.0	25	4	US-09-004-838-26	Sequence 26, Appl	C 916	25	10.0	42	3	US-09-131-009A-14	Sequence 14, Appl
C 844	25	10.0	25	4	US-09-004-838-26	Sequence 26, Appl	C 917	25	10.0	42	3	US-09-092-226A-14	Sequence 14, Appl
C 845	25	10.0	25	4	US-07-868-539C-18	Sequence 18, Appl	C 918	25	10.0	42	3	US-09-130-862A-14	Sequence 14, Appl
C 846	25	10.0	25	4	US-07-868-539C-18	Sequence 18, Appl	C 919	25	10.0	42	3	US-09-090-809A-14	Sequence 14, Appl
C 847	25	10.0	28	1	US-07-976-103A-50	Sequence 50, Appl	C 920	25	10.0	42	4	US-08-679-493A-55	Sequence 55, Appl
C 848	25	10.0	28	1	US-07-976-103A-50	Sequence 50, Appl	C 921	25	10.0	42	4	US-09-053-116A-14	Sequence 14, Appl
C 849	25	10.0	28	2	US-08-473-481-50	Sequence 50, Appl	C 922	25	10.0	43	3	US-09-275-850-44	Sequence 44, Appl
C 850	25	10.0	28	2	US-08-473-481-50	Sequence 50, Appl	C 923	25	10.0	43	3	US-09-275-850-44	Sequence 44, Appl
C 851	25	10.0	28	3	US-08-779-355-21	Sequence 21, Appl	C 924	25	10.0	44	2	US-08-659-453B-22	Sequence 22, Appl
C 852	25	10.0	28	3	US-08-779-355-21	Sequence 21, Appl	C 925	25	10.0	44	2	US-09-089-853A-22	Sequence 22, Appl
C 853	25	10.0	28	3	US-08-938-835A-21	Sequence 21, Appl	C 926	25	10.0	44	3	US-09-131-009A-22	Sequence 22, Appl
C 854	25	10.0	28	3	US-08-938-835A-21	Sequence 21, Appl	C 927	25	10.0	44	3	US-09-092-226A-22	Sequence 22, Appl
C 855	25	10.0	28	4	US-08-599-738A-50	Sequence 50, Appl	C 928	25	10.0	44	3	US-09-130-862A-22	Sequence 22, Appl
C 856	25	10.0	28	4	US-08-599-738A-50	Sequence 50, Appl	C 929	25	10.0	44	3	US-09-090-809A-22	Sequence 22, Appl
C 857	25	10.0	29	1	US-08-162-590A-1	Sequence 1, Appli	C 930	25	10.0	44	4	US-09-053-116A-22	Sequence 22, Appl
C 858	25	10.0	29	1	US-08-162-590A-1	Sequence 1, Appli	C 931	25	10.0	45	3	US-08-180-470-76	Sequence 76, Appl
C 859	25	10.0	29	1	US-08-162-590A-2	Sequence 2, Appli	C 932	25	10.0	46	4	US-08-974-549A-534	Sequence 534, App
C 860	25	10.0	29	1	US-08-162-590A-2	Sequence 2, Appli	C 933	25	10.0	46	4	US-08-912-951-301	Sequence 301, App
C 861	25	10.0	29	1	US-08-162-590A-3	Sequence 3, Appli	C 934	25	10.0	46	4	US-09-301-721A-2	Sequence 2, Appli
C 862	25	10.0	29	1	US-08-162-590A-3	Sequence 3, Appli	C 935	25	10.0	46	4	US-09-301-721A-2	Sequence 2, Appli
C 863	25	10.0	29	1	US-08-372-556-8	Sequence 8, Appli	C 936	25	10.0	47	2	US-08-769-945C-7	Sequence 7, Appli
C 864	25	10.0	29	1	US-08-372-556-8	Sequence 8, Appli	C 937	25	10.0	47	2	US-08-769-945C-7	Sequence 7, Appli
C 865	25	10.0	30	1	US-08-372-556-7	Sequence 7, Appli	C 938	25	10.0	47	2	US-08-769-945C-8	Sequence 8, Appli
C 866	25	10.0	30	1	US-08-372-556-7	Sequence 7, Appli	C 939	25	10.0	47	2	US-08-769-945C-8	Sequence 8, Appli
C 867	25	10.0	30	3	US-08-892-747-7	Sequence 7, Appli	C 940	25	10.0	50	1	US-07-931-473B-54	Sequence 54, Appl
C 868	25	10.0	30	3	US-08-892-747-7	Sequence 7, Appli	C 941	25	10.0	50	1	US-07-931-473B-54	Sequence 54, Appl
C 869	25	10.0	30	4	US-09-083-123-6	Sequence 6, Appli	C 942	25	10.0	50	1	US-07-714-131C-54	Sequence 54, Appl
C 870	25	10.0	30	4	US-09-083-123-6	Sequence 6, Appli	C 943	25	10.0	50	1	US-07-714-131C-54	Sequence 54, Appl
C 871	25	10.0	33	1	US-08-162-590A-9	Sequence 9, Appli	C 944	25	10.0	50	1	US-08-412-110-54	Sequence 54, Appl
C 872	25	10.0	33	1	US-08-162-590A-9	Sequence 9, Appli	C 945	25	10.0	50	1	US-08-412-110-54	Sequence 54, Appl
C 873	25	10.0	33	1	US-08-162-590A-10	Sequence 10, Appl	C 946	25	10.0	50	1	US-08-409-442A-54	Sequence 54, Appl
C 874	25	10.0	33	1	US-08-162-590A-10	Sequence 10, Appl	C 947	25	10.0	50	1	US-08-409-442A-54	Sequence 54, Appl
C 875	25	10.0	34	3	US-08-974-549A-531	Sequence 531, App	C 948	25	10.0	50	1	US-08-409-442A-533	Sequence 533, App
C 876	25	10.0	34	3	US-08-974-549A-532	Sequence 532, App	C 949	25	10.0	50	1	US-08-409-442A-533	Sequence 533, App
C 877	25	10.0	34	3	US-08-974-549A-532	Sequence 532, App	C 950	25	10.0	50	2	US-08-469-609A-54	Sequence 54, Appl
C 878	25	10.0	34	4	US-09-364-539-11	Sequence 11, Appl	C 951	25	10.0	50	2	US-08-469-609A-54	Sequence 54, Appl
C 879	25	10.0	34	4	US-09-364-539-11	Sequence 11, Appl	C 952	25	10.0	50	2	US-08-469-609A-533	Sequence 533, App
C 880	25	10.0	34	4	US-08-912-951-298	Sequence 298, App	C 953	25	10.0	50	2	US-08-469-609A-533	Sequence 533, App
C 881	25	10.0	34	4	US-08-912-951-299	Sequence 299, App	C 954	25	10.0	50	3	US-09-143-190-54	Sequence 54, Appl
C 882	25	10.0	34	4	US-08-912-951-299	Sequence 299, App	C 955	25	10.0	50	3	US-09-143-190-54	Sequence 54, Appl
C 883	25	10.0	37	1	US-08-162-590A-5	Sequence 5, Appli	C 956	25	10.0	50	3	US-09-143-190-353	Sequence 353, App
C 884	25	10.0	37	1	US-08-162-590A-5	Sequence 5, Appli	C 957	25	10.0	50	3	US-09-143-190-353	Sequence 353, App
C 885	25	10.0	37	1	US-08-162-590A-6	Sequence 6, Appli	C 958	25	10.0	50	3	US-09-593-323-26	Sequence 26, Appl
C 886	25	10.0	37	1	US-08-162-590A-6	Sequence 6, Appli	C 959	25	10.0	50	3	US-09-593-323-26	Sequence 26, Appl
C 887	25	10.0	37	1	US-08-162-590A-7	Sequence 7, Appli	C 960	25	10.0	50	3	US-09-594-108-26	Sequence 26, Appl
C 888	25	10.0	37	1	US-08-162-590A-7	Sequence 7, Appli	C 961	25	10.0	50	3	US-09-594-108-26	Sequence 26, Appl
C 889	25	10.0	37	1	US-08-162-590A-8	Sequence 8, Appli	C 962	25	10.0	50	3	US-09-344-300-26	Sequence 26, Appl
C 890	25	10.0	37	1	US-08-162-590A-8	Sequence 8, Appli	C 963	25	10.0	50	3	US-09-344-300-26	Sequence 26, Appl
C 891	25	10.0	38	3	US-09-275-850-336	Sequence 336, App	C 964	25	10.0	50	4	US-09-502-344-54	Sequence 54, Appl
C 892	25	10.0	38	3	US-09-275-850-336	Sequence 336, App	C 965	25	10.0	50	4	US-09-502-344-54	Sequence 54, Appl
C 893	25	10.0	38	3	US-09-275-850-337	Sequence 337, App	C 966	25	10.0	50	4	US-09-502-344-54	Sequence 54, Appl
C 894	25	10.0	38	3	US-09-275-850-337	Sequence 337, App	C 967	25	10.0	50	4	US-09-502-344-353	Sequence 353, App
C 895	25	10.0	39	1	US-08-575-361A-19	Sequence 19, Appl	C 968	25	10.0	51	3	US-09-275-850-179	Sequence 179, App
C 896	25	10.0	39	1	US-08-575-361A-20	Sequence 20, Appl	C 969	25	10.0	51	3	US-09-275-850-179	Sequence 179, App
C 897	25	10.0	39	2	US-08-659-453B-2	Sequence 2, Appli	C 970	25	10.0	52	3	US-08-974-549A-535	Sequence 535, App
C 898	25	10.0	39	2	US-08-659-453B-2	Sequence 2, Appli	C 971	25	10.0	52	3	US-08-974-549A-535	Sequence 535, App
C 899	25	10.0	39	3	US-09-131-009A-2	Sequence 2, Appli	C 972	25	10.0	52	4	US-09-916-228-29	Sequence 29, Appl
C 900	25	10.0	39	3	US-09-131-009A-2	Sequence 2, Appli	C 973	25	10.0	52	4	US-09-916-228-29	Sequence 29, Appl
C 901	25	10.0	39	3	US-09-130-862A-2	Sequence 2, Appli	C 974	25	10.0	54	4	US-09-504-132-9	Sequence 9, Appli
C 902	25	10.0	39	3	US-09-130-862A-2	Sequence 2, Appli	C 975	25	10.0	55	3	US-09-275-850-333	Sequence 333, App
C 903	25	10.0	39	3	US-09-090-809A-2	Sequence 2, Appli	C 976	25	10.0	55	3	US-09-275-850-333	Sequence 333, App

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977      25 10.0 55 3 US-09-275-850-334
c 978      25 10.0 55 3 US-09-275-850-334
979      25 10.0 55 3 US-09-275-850-335
c 980      25 10.0 55 3 US-09-275-850-335
981      25 10.0 56 2 US-08-432-871C-3
c 982      25 10.0 56 2 US-08-432-871C-3
983      25 10.0 56 4 US-09-270-956-3
c 984      25 10.0 56 4 US-09-270-956-3
985      25 10.0 57 2 US-08-136-214-8
c 986      25 10.0 57 2 US-08-136-214-8
c 987      25 10.0 58 3 US-08-974-549A-536
c 988      25 10.0 58 4 US-08-912-951-303
c 989      25 10.0 59 1 US-07-964-624D-13
c 990      25 10.0 59 1 US-08-442-062-13
991      25 10.0 60 2 US-09-004-192A-11
c 992      25 10.0 60 2 US-09-004-192A-11
c 993      25 10.0 60 3 US-09-150-805-1
c 994      25 10.0 60 3 US-08-996-069A-1
c 995      25 10.0 60 4 US-09-083-123-1
c 996      25 10.0 61 2 US-08-792-075-1
c 997      25 10.0 61 2 US-08-792-075-1
c 998      25 10.0 61 3 US-09-046-247-2
c 999      25 10.0 61 3 US-09-046-247-2
1000     25 10.0 61 3 US-08-870-930-10

ALIGNMENTS

RESULT 1
US-08-837-199A-21/c
; Sequence 21, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(445)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1075)
; OTHER INFORMATION: No. 6455277e= "1 to 1075 is 1255 to 2330 of Figure 5 Hsgr-2"
; NAME/KEY: misc_feature
; LOCATION: (763)..(801)
; OTHER INFORMATION: N in position 763 to 801 indicates positions of divergence between
; OTHER INFORMATION: n different receptor clones.
; US-08-837-199A-21

Query Match 12.4%; Score 31; DB 4; Length 1075;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
   |||||
2b 807 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 777
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```

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RESULT 2
US-08-837-199A-46/c
; Sequence 46, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (586)..(586)
; OTHER INFORMATION: N in position 586 indicates a position of divergence between di
; OTHER INFORMATION: erent receptor clones.
; NAME/KEY: misc_feature
; LOCATION: (764)..(802)
; OTHER INFORMATION: N in positions 764 to 802 indicates positions of divergence be
; OTHER INFORMATION: een different receptor clones.
; US-08-837-199A-46

Query Match 12.4%; Score 31; DB 4; Length 1076;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
   |||||
Db 808 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 778
   |||||

RESULT 3
US-08-837-199A-15/c
; Sequence 15, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 2157
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(886)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2157)
; OTHER INFORMATION: No. 6455277e= "1 to 2157 is 814 to 2971 of Figure 5 29brc"
; NAME/KEY: misc_feature
; LOCATION: (1204)..(1242)
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OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif  
OTHER INFORMATION: feret receptor clones  
NAME/KEY: misc feature  
LOCATION: (2256)..(2294)  
OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence bet  
OTHER INFORMATION: ween different receptor clones  
NAME/KEY: misc feature  
LOCATION: (1091)..(1091)  
OTHER INFORMATION: N in position 1091 indicates any nucleic acid  
US-08-837-199A-5

Query Match 12.4%; Score 31; DB 4; Length 3209;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
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Db 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

## RESULT 7

US-08-837-199A-37/c  
Sequence 37, Application US/08837199A  
Patent No. 6455277  
GENERAL INFORMATION:  
APPLICANT: FOX, GARY M.  
APPLICANT: JING, SHUQIAN  
APPLICANT: WEN, DUANZHI  
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR  
FILE REFERENCE: A-401C  
CURRENT APPLICATION NUMBER: US/08/837,199A  
CURRENT FILING DATE: 1997-04-14  
PRIOR APPLICATION NUMBER: US 60/015,907  
PRIOR FILING DATE: 1996-04-22  
PRIOR APPLICATION NUMBER: US 60/017,221  
PRIOR FILING DATE: 1996-05-09  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 37  
LENGTH: 3209  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1091)..(1091)  
OTHER INFORMATION: N in position 1091 indicates any nucleic acid.  
NAME/KEY: misc feature  
LOCATION: (2078)..(2078)  
OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif  
OTHER INFORMATION: feret receptor clones.  
NAME/KEY: misc feature  
LOCATION: (2256)..(2294)  
OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence bet  
OTHER INFORMATION: ween different receptor clones.  
US-08-837-199A-37

Query Match 12.4%; Score 31; DB 4; Length 3209;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
|||||  
Db 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

## RESULT 8

US-09-867-915-27  
Sequence 27, Application US/09867915  
Patent No. 6521747  
GENERAL INFORMATION:  
APPLICANT: Genaisance Pharmaceuticals, Inc.  
APPLICANT: Anastasio, Allison E.  
APPLICANT: Finkel, Kevin

APPLICANT: Koshy, Beena  
APPLICANT: Lee, Helen H.  
TITLE OF INVENTION: HAPLOTYPES OF THE AGTR1 GENE  
FILE REFERENCE: AGTR1-1136test  
CURRENT APPLICATION NUMBER: US/09/867,915  
CURRENT FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: 60/228,542  
PRIOR FILING DATE: 2000-08-28  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 27  
LENGTH: 780  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: (30)  
OTHER INFORMATION: PS1: polymorphic base T or A  
NAME/KEY:  
LOCATION: (61)..(120)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (150)  
OTHER INFORMATION: PS2: polymorphic base G or T  
NAME/KEY:  
LOCATION: (181)..(240)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (270)  
OTHER INFORMATION: PS3: polymorphic base T or C  
NAME/KEY:  
LOCATION: (301)..(360)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (390)  
OTHER INFORMATION: PS4: polymorphic base T or C  
NAME/KEY:  
LOCATION: (421)..(480)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (510)  
OTHER INFORMATION: PS5: polymorphic base C or T  
NAME/KEY:  
LOCATION: (541)..(600)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (630)  
OTHER INFORMATION: PS6: polymorphic base A or G  
NAME/KEY:  
LOCATION: (661)..(720)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (750)  
OTHER INFORMATION: PS7: polymorphic base T or G  
US-09-867-915-27

Query Match 12.0%; Score 30; DB 4; Length 780;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCA 129  
|||||  
Db 216 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCA 245

## RESULT 9

US-09-484-970B-26/c  
Sequence 26, Application US/09484970B  
Patent No. 6426186  
GENERAL INFORMATION:  
APPLICANT: Jones, Karen A.  
APPLICANT: Volkmuth, Wayne  
APPLICANT: Walker, Michael G.



```
/ TELEFAX: (617) 861-9540
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13999 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
/ MOLECULE TYPE: DNA (genomic)
/ IMMEDIATE SOURCE:
/ CLONE: PAG4611
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..13999
/ OTHER INFORMATION: /note= "Function = "Expression
/ OTHER INFORMATION: Vector Coding Sequence"
/
US-08-444-644-24

Query Match 11.6%; Score 29; DB 3; Length 13999;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 AATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
Db 11461 AATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 11433

RESULT 13
JS-08-232-246A-24/c
Sequence 24, Application US/08232246A
Patent No. 6329508
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/600,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 13999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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/ TOPOLOGY: circular
/ MOLECULE TYPE: DNA (genomic)
/ IMMEDIATE SOURCE:
/ CLONE: PAG4611
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..13999
/ OTHER INFORMATION: /note= "Function = "Expression
/ OTHER INFORMATION: Vector Coding Sequence"
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US-08-232-246A-24

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Best Local Similarity 100.0%; Pred. No. 4.7e-06;
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Db 11461 AATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 11433

RESULT 14
US-09-804-471A-3
Sequence 3, Application US/09804471A
Patent No. 6479269
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 174493
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(174493)
OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match 11.6%; Score 29; DB 4; Length 174493;
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RESULT 15
US-09-645-629-31
Sequence 31, Application US/09645629
Patent No. 6472515
GENERAL INFORMATION:
APPLICANT: Climent-Johansson, Isabel
APPLICANT: Dahlman-Wright, Karin
APPLICANT: Lake, Staffan
APPLICANT: Wasserman, Wyeth
TITLE OF INVENTION: NOVEL RESPONSE ELEMENT
FILE REFERENCE: 13425-012001
CURRENT APPLICATION NUMBER: US/09/645,629
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: SE 9904269-9
PRIOR FILING DATE: 1999-11-25
PRIOR APPLICATION NUMBER: US 60/151,867
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: SE 9903009-0
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 34
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for DNA binding site selection
; NAME/KEY: misc feature
; LOCATION: (1)..(65)
; OTHER INFORMATION: n = A,T,C or G
; US-09-645-629-31

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GenCore version 5.1.6  
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CM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 04:14:30 ; Search time 1046 Seconds  
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Perfect score: 251  
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Scoring table: OLIGO NJC  
Gapop 60.0 , Gapext 60.0

Searched: 2141354 seqs, 1595478879 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 243	28	11.2	175590	11	US-09-911-077A-13	Sequence 13, Appl	C 316	27	10.8	65	12	US-09-230-111C-33	Sequence 33, Appl
C 244	28	11.2	175590	11	US-09-911-077A-13	Sequence 13, Appl	C 317	27	10.8	65	14	US-10-224-836-87	Sequence 87, Appl
C 245	28	11.2	197997	10	US-09-822-246-3	Sequence 3, Appl	C 318	27	10.8	66	9	US-09-766-113-9	Sequence 9, Appl
C 246	28	11.2	215980	11	US-09-972-546-16	Sequence 16, Appl	C 319	27	10.8	66	14	US-10-224-836-88	Sequence 88, Appl
C 247	28	11.2	250000	12	US-10-225-810-26	Sequence 26, Appl	C 320	27	10.8	67	14	US-10-224-836-89	Sequence 89, Appl
C 248	28	11.2	254366	11	US-09-822-871-3	Sequence 3, Appl	C 321	27	10.8	68	14	US-10-224-836-90	Sequence 90, Appl
C 249	28	11.2	263744	12	US-10-329-834A-6	Sequence 6, Appl	C 322	27	10.8	69	12	US-10-164-515-4	Sequence 4, Appl
C 250	28	11.2	322101	12	US-10-060-902-1	Sequence 1, Appl	C 323	27	10.8	69	14	US-10-224-836-91	Sequence 91, Appl
C 251	28	11.2	326014	9	US-09-731-231A-3	Sequence 3, Appl	C 324	27	10.8	70	14	US-10-224-836-92	Sequence 92, Appl
C 252	28	11.2	378361	11	US-09-901-136-3	Sequence 3, Appl	C 325	27	10.8	71	14	US-10-224-836-93	Sequence 93, Appl
C 253	28	11.2	392000	12	US-10-227-983-11	Sequence 11, Appl	C 326	27	10.8	72	9	US-09-790-399-5	Sequence 5, Appl
C 254	28	11.2	786431	12	US-10-412-277-3	Sequence 3, Appl	C 327	27	10.8	72	12	US-10-008-524A-174	Sequence 174, App
C 255	27	10.8	28	14	US-10-224-836-50	Sequence 50, Appl	C 328	27	10.8	72	14	US-10-224-836-94	Sequence 94, Appl
C 256	27	10.8	29	14	US-10-224-836-51	Sequence 51, Appl	C 329	27	10.8	73	12	US-10-008-524A-178	Sequence 178, App
C 257	27	10.8	30	14	US-10-224-836-52	Sequence 52, Appl	C 330	27	10.8	73	14	US-10-077-319-1	Sequence 1, Appl
C 258	27	10.8	31	14	US-10-224-836-53	Sequence 53, Appl	C 331	27	10.8	73	14	US-10-224-836-95	Sequence 95, Appl
C 259	27	10.8	32	14	US-10-224-836-54	Sequence 54, Appl	C 332	27	10.8	74	14	US-10-224-836-96	Sequence 96, Appl
C 260	27	10.8	33	14	US-10-224-836-55	Sequence 55, Appl	C 333	27	10.8	75	10	US-09-833-381-884	Sequence 884, App
C 261	27	10.8	34	12	US-09-132-231-36	Sequence 36, Appl	C 334	27	10.8	75	14	US-10-224-836-97	Sequence 97, Appl
C 262	27	10.8	34	14	US-10-224-836-56	Sequence 56, Appl	C 335	27	10.8	76	11	US-09-860-474-57	Sequence 57, Appl
C 263	27	10.8	34	14	US-10-044-692-298	Sequence 298, App	C 336	27	10.8	76	12	US-10-409-565-57	Sequence 57, Appl
C 264	27	10.8	35	14	US-10-044-539-298	Sequence 298, App	C 337	27	10.8	76	14	US-10-224-836-98	Sequence 98, Appl
C 265	27	10.8	35	14	US-10-224-836-57	Sequence 57, Appl	C 338	27	10.8	77	11	US-09-860-474-1	Sequence 1, Appl
C 266	27	10.8	36	12	US-10-330-772-26	Sequence 26, Appl	C 339	27	10.8	77	11	US-09-916-443A-4	Sequence 4, Appl
C 267	27	10.8	36	12	US-10-330-772-26	Sequence 26, Appl	C 340	27	10.8	77	12	US-10-037-986-38	Sequence 38, Appl
C 268	27	10.8	37	14	US-10-224-836-58	Sequence 58, Appl	C 341	27	10.8	77	12	US-10-409-565-1	Sequence 1, Appl
C 269	27	10.8	37	14	US-10-224-836-59	Sequence 59, Appl	C 342	27	10.8	77	12	US-09-974-330-1	Sequence 1, Appl
C 270	27	10.8	38	14	US-10-224-836-60	Sequence 60, Appl	C 343	27	10.8	77	12	US-10-408-085-38	Sequence 38, Appl
C 271	27	10.8	39	14	US-10-224-836-61	Sequence 61, Appl	C 344	27	10.8	77	14	US-10-224-836-99	Sequence 99, Appl
C 272	27	10.8	40	11	US-09-907-111-348	Sequence 348, App	C 345	27	10.8	78	9	US-09-908-130-1	Sequence 1, Appl
C 273	27	10.8	40	14	US-10-224-836-62	Sequence 62, Appl	C 346	27	10.8	78	9	US-09-908-131-1	Sequence 1, Appl
C 274	27	10.8	40	14	US-10-044-692-300	Sequence 300, App	C 347	27	10.8	78	10	US-09-907-795-1	Sequence 1, Appl
C 275	27	10.8	40	14	US-10-224-836-63	Sequence 63, Appl	C 348	27	10.8	78	10	US-10-124-884-1	Sequence 1, Appl
C 276	27	10.8	41	14	US-10-224-836-64	Sequence 64, Appl	C 349	27	10.8	78	14	US-10-224-836-100	Sequence 100, App
C 277	27	10.8	42	14	US-10-330-772-44	Sequence 44, Appl	C 350	27	10.8	79	14	US-10-224-836-101	Sequence 101, App
C 278	27	10.8	43	12	US-10-330-772-44	Sequence 44, Appl	C 351	27	10.8	80	14	US-10-224-836-102	Sequence 102, App
C 279	27	10.8	43	12	US-10-330-772-44	Sequence 44, Appl	C 352	27	10.8	81	14	US-10-224-836-103	Sequence 103, App
C 280	27	10.8	44	14	US-10-224-836-65	Sequence 65, Appl	C 353	27	10.8	82	13	US-10-097-171-6	Sequence 6, Appl
C 281	27	10.8	44	14	US-10-224-836-66	Sequence 66, Appl	C 354	27	10.8	82	14	US-10-224-836-104	Sequence 104, App
C 282	27	10.8	45	14	US-10-224-836-67	Sequence 67, Appl	C 355	27	10.8	83	14	US-10-224-836-105	Sequence 105, App
C 283	27	10.8	46	14	US-10-224-836-68	Sequence 68, Appl	C 356	27	10.8	84	14	US-10-224-836-106	Sequence 106, App
C 284	27	10.8	46	14	US-10-044-692-301	Sequence 301, App	C 357	27	10.8	85	14	US-10-224-836-107	Sequence 107, App
C 285	27	10.8	47	14	US-10-224-836-69	Sequence 69, Appl	C 358	27	10.8	86	10	US-09-781-902-63	Sequence 63, Appl
C 286	27	10.8	48	12	US-10-021-718-4	Sequence 4, Appl	C 359	27	10.8	86	14	US-10-224-836-108	Sequence 108, App
C 287	27	10.8	48	14	US-10-224-836-70	Sequence 70, Appl	C 360	27	10.8	87	11	US-09-916-443A-2	Sequence 2, Appl
C 288	27	10.8	48	14	US-10-021-577-4	Sequence 4, Appl	C 361	27	10.8	87	12	US-10-223-666-49	Sequence 49, Appl
C 289	27	10.8	49	14	US-10-224-836-71	Sequence 71, Appl	C 362	27	10.8	87	12	US-10-223-666-52	Sequence 52, Appl
C 290	27	10.8	50	14	US-10-224-836-72	Sequence 72, Appl	C 363	27	10.8	87	13	US-10-096-830-44	Sequence 44, Appl
C 291	27	10.8	50	14	US-10-224-836-72	Sequence 72, Appl	C 364	27	10.8	87	14	US-10-224-836-109	Sequence 109, App
C 292	27	10.8	51	14	US-10-224-836-73	Sequence 73, Appl	C 365	27	10.8	88	14	US-10-224-836-110	Sequence 110, App
C 293	27	10.8	52	14	US-10-028-396A-5	Sequence 5, Appl	C 366	27	10.8	89	14	US-10-224-836-111	Sequence 111, App
C 294	27	10.8	52	14	US-10-224-836-74	Sequence 74, Appl	C 367	27	10.8	90	10	US-09-780-929-100	Sequence 100, App
C 295	27	10.8	52	14	US-10-044-692-302	Sequence 302, App	C 368	27	10.8	90	12	US-10-008-524A-177	Sequence 177, App
C 296	27	10.8	52	14	US-10-044-539-302	Sequence 302, App	C 369	27	10.8	90	14	US-10-224-836-112	Sequence 112, App
C 297	27	10.8	53	14	US-10-224-836-75	Sequence 75, Appl	C 370	27	10.8	91	14	US-10-224-836-113	Sequence 113, App
C 298	27	10.8	54	14	US-10-224-836-76	Sequence 76, Appl	C 371	27	10.8	92	14	US-10-224-836-114	Sequence 114, App
C 299	27	10.8	55	14	US-10-224-836-77	Sequence 77, Appl	C 372	27	10.8	93	14	US-10-224-836-115	Sequence 115, App
C 300	27	10.8	56	14	US-10-224-836-78	Sequence 78, Appl	C 373	27	10.8	94	14	US-10-224-836-116	Sequence 116, App
C 301	27	10.8	57	14	US-10-224-836-79	Sequence 79, Appl	C 374	27	10.8	95	14	US-10-224-836-117	Sequence 117, App
C 302	27	10.8	58	14	US-10-224-836-80	Sequence 80, Appl	C 375	27	10.8	96	11	US-09-851-486-36	Sequence 36, Appl
C 303	27	10.8	58	14	US-10-044-692-303	Sequence 303, App	C 376	27	10.8	96	12	US-10-223-666-125	Sequence 125, App
C 304	27	10.8	59	14	US-10-044-539-303	Sequence 303, App	C 377	27	10.8	96	14	US-10-224-836-118	Sequence 118, App
C 305	27	10.8	59	14	US-10-224-836-81	Sequence 81, Appl	C 378	27	10.8	97	10	US-09-780-929-102	Sequence 102, App
C 306	27	10.8	60	12	US-10-269-031A-124	Sequence 124, App	C 379	27	10.8	97	11	US-09-849-928-248	Sequence 248, App
C 307	27	10.8	60	14	US-10-224-836-82	Sequence 82, Appl	C 380	27	10.8	97	11	US-09-849-928-390	Sequence 390, App
C 308	27	10.8	61	11	US-09-907-111-344	Sequence 344, App	C 381	27	10.8	97	14	US-10-066-960-248	Sequence 248, App

C 382	27	10.8	97	14	US-10-066-360-390	Sequence 390, App	455	27	10.8	431	12	US-10-027-632-253666	Sequence 253666,
C 383	27	10.8	97	14	US-10-224-836-119	Sequence 119, App	456	27	10.8	431	13	US-10-027-632-253666	Sequence 253666,
C 384	27	10.8	98	14	US-10-224-836-120	Sequence 120, App	c 457	27	10.8	434	11	US-09-910-082A-117	Sequence 117, App
C 385	27	10.8	99	14	US-10-224-836-121	Sequence 121, App	c 458	27	10.8	436	12	US-09-814-353-5048	Sequence 5048, Ap
C 386	27	10.8	100	14	US-10-224-836-122	Sequence 122, App	c 459	27	10.8	436	12	US-09-814-353-11340	Sequence 11340, A
C 387	27	10.8	101	14	US-10-224-836-123	Sequence 123, App	c 460	27	10.8	441	12	US-09-814-353-20405	Sequence 20405, A
C 388	27	10.8	102	14	US-10-224-836-124	Sequence 124, App	c 461	27	10.8	448	12	US-09-814-353-20466	Sequence 20466, A
C 389	27	10.8	103	11	US-09-952-680A-4	Sequence 4, Appli	c 462	27	10.8	451	11	US-09-918-995-24108	Sequence 24108, A
C 390	27	10.8	103	14	US-10-224-836-125	Sequence 125, App	c 463	27	10.8	455	11	US-09-918-995-15038	Sequence 15038, A
C 391	27	10.8	104	13	US-10-224-997-1	Sequence 1, Appli	c 464	27	10.8	455	12	US-09-814-353-5293	Sequence 5293, Ap
C 392	27	10.8	104	14	US-10-224-836-126	Sequence 126, App	c 465	27	10.8	455	12	US-09-814-353-11580	Sequence 11580, A
C 393	27	10.8	105	14	US-10-224-836-127	Sequence 127, App	c 466	27	10.8	462	11	US-08-918-995-14241	Sequence 14241, A
C 394	27	10.8	106	14	US-10-224-836-128	Sequence 128, App	c 467	27	10.8	462	11	US-08-918-995-19257	Sequence 19257, A
C 395	27	10.8	107	14	US-10-224-836-129	Sequence 129, App	c 468	27	10.8	467	12	US-10-082-828A-138	Sequence 138, App
C 396	27	10.8	108	14	US-10-224-836-130	Sequence 130, App	c 469	27	10.8	470	12	US-10-027-632-260668	Sequence 260668,
C 397	27	10.8	109	14	US-10-224-836-131	Sequence 131, App	c 470	27	10.8	470	12	US-10-027-632-260669	Sequence 260669,
C 398	27	10.8	110	9	US-09-815-171A-14	Sequence 14, Appli	c 471	27	10.8	470	13	US-10-027-632-260668	Sequence 260668,
C 399	27	10.8	110	9	US-09-815-171A-14	Sequence 14, Appli	c 472	27	10.8	470	13	US-10-027-632-260669	Sequence 260669,
C 400	27	10.8	110	14	US-10-224-836-132	Sequence 132, App	c 473	27	10.8	472	11	US-09-918-995-29274	Sequence 29274, A
C 401	27	10.8	111	14	US-10-224-836-133	Sequence 133, App	c 474	27	10.8	474	11	US-09-918-995-11062	Sequence 11062, A
C 402	27	10.8	112	14	US-10-224-836-134	Sequence 134, App	c 475	27	10.8	477	11	US-09-918-995-20420	Sequence 20420, A
C 403	27	10.8	113	14	US-10-224-836-135	Sequence 135, App	c 476	27	10.8	478	12	US-10-027-632-270575	Sequence 270575,
C 404	27	10.8	114	14	US-10-224-836-136	Sequence 136, App	c 477	27	10.8	478	13	US-10-027-632-270575	Sequence 270575,
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C 406	27	10.8	123	10	US-09-781-902-55	Sequence 55, Appli	c 479	27	10.8	484	11	US-09-918-995-23299	Sequence 23299, A
C 407	27	10.8	147	11	US-09-936-443A-6	Sequence 6, Appli	c 480	27	10.8	486	11	US-09-918-995-23155	Sequence 23155, A
C 408	27	10.8	147	11	US-09-916-443A-7	Sequence 7, Appli	c 481	27	10.8	486	11	US-09-918-995-23155	Sequence 23155, A
C 409	27	10.8	147	11	US-09-916-443A-7	Sequence 7, Appli	c 482	27	10.8	486	12	US-09-814-353-1784	Sequence 1784, Ap
C 410	27	10.8	154	10	US-09-884-566-7	Sequence 6037, Ap	c 483	27	10.8	486	12	US-09-814-353-5206	Sequence 5206, Ap
C 411	27	10.8	159	9	US-09-923-876-6037	Sequence 1319, Ap	c 484	27	10.8	486	12	US-09-814-353-8132	Sequence 8132, Ap
C 412	27	10.8	224	9	US-09-923-876-1319	Sequence 5344, Ap	c 485	27	10.8	486	12	US-09-814-353-11493	Sequence 11493, A
C 413	27	10.8	233	9	US-09-294-093B-5344	Sequence 2442, Ap	c 486	27	10.8	486	14	US-10-198-846-14035	Sequence 14035, A
C 414	27	10.8	245	9	US-09-923-876-2342	Sequence 1205, Ap	c 487	27	10.8	487	14	US-10-034-934-30	Sequence 30, Appli
C 415	27	10.8	247	9	US-09-294-093B-1205	Sequence 1205, Ap	c 488	27	10.8	488	11	US-09-918-995-1622	Sequence 1622, Ap
C 416	27	10.8	256	9	US-09-923-876-388	Sequence 583, App	c 489	27	10.8	488	11	US-09-918-995-15307	Sequence 15307, A
C 417	27	10.8	258	9	US-09-923-876-593	Sequence 583, App	c 490	27	10.8	488	11	US-09-918-995-20849	Sequence 20849, A
C 418	27	10.8	258	9	US-09-923-876-593	Sequence 583, App	c 491	27	10.8	488	11	US-09-918-995-22476	Sequence 22476, A
C 419	27	10.8	263	9	US-09-923-876-2037	Sequence 2037, Ap	c 492	27	10.8	490	11	US-09-918-995-23760	Sequence 23760, A
C 420	27	10.8	269	9	US-09-923-876-160	Sequence 160, App	c 493	27	10.8	490	11	US-09-918-995-24758	Sequence 24758, A
C 421	27	10.8	272	9	US-09-923-876-5522	Sequence 5522, Ap	c 494	27	10.8	492	14	US-10-198-846-10882	Sequence 10882, A
C 422	27	10.8	278	12	US-10-027-632-177885	Sequence 177885,	c 495	27	10.8	493	10	US-09-736-457-13	Sequence 13, Appli
C 423	27	10.8	278	13	US-10-027-632-177885	Sequence 177885,	c 496	27	10.8	493	10	US-09-902-941-13	Sequence 13, Appli
C 424	27	10.8	282	9	US-09-294-093B-3390	Sequence 3390, Ap	c 497	27	10.8	493	10	US-09-849-626-13	Sequence 20998, A
C 425	27	10.8	282	13	US-10-016-634A-30	Sequence 30, Appli	c 498	27	10.8	493	11	US-09-918-995-20998	Sequence 20998, A
C 426	27	10.8	283	9	US-09-923-876-5486	Sequence 5486, Ap	c 499	27	10.8	493	11	US-09-476-300-13	Sequence 13, Appli
C 427	27	10.8	284	14	US-10-011-585A-4	Sequence 4, Appli	c 500	27	10.8	493	12	US-10-113-872-13	Sequence 13, Appli
C 428	27	10.8	290	9	US-09-294-093B-399	Sequence 399, App	c 501	27	10.8	493	14	US-10-017-754-13	Sequence 13, Appli
C 429	27	10.8	301	10	US-09-833-381-1013	Sequence 1013, Ap	c 502	27	10.8	495	11	US-09-918-995-27206	Sequence 27206, A
C 430	27	10.8	311	10	US-09-833-381-1014	Sequence 1014, Ap	c 503	27	10.8	495	12	US-09-814-353-5212	Sequence 5212, Ap
C 431	27	10.8	327	14	US-10-198-846-10739	Sequence 10739, A	c 504	27	10.8	495	12	US-09-814-353-11499	Sequence 11499, A
C 432	27	10.8	345	10	US-09-999-025-16	Sequence 16, Appli	c 505	27	10.8	496	11	US-09-918-995-20853	Sequence 20853, A
C 433	27	10.8	345	10	US-09-999-040-16	Sequence 16, Appli	c 506	27	10.8	496	13	US-10-016-157A-128	Sequence 128, App
C 434	27	10.8	345	11	US-09-998-817-16	Sequence 17, Appli	c 507	27	10.8	502	11	US-09-918-995-1333	Sequence 1333, Ap
C 435	27	10.8	345	11	US-09-999-021-16	Sequence 16, Appli	c 508	27	10.8	504	14	US-10-198-846-12886	Sequence 12886, A
C 436	27	10.8	345	12	US-09-814-353-854	Sequence 854, App	c 509	27	10.8	506	11	US-09-918-995-12867	Sequence 12867, A
C 437	27	10.8	345	12	US-09-814-353-7226	Sequence 7226, Ap	c 510	27	10.8	506	11	US-09-918-995-19851	Sequence 19851, A
C 438	27	10.8	345	14	US-10-040-997-16	Sequence 16, Appli	c 511	27	10.8	509	11	US-09-918-995-23157	Sequence 23157, A
C 439	27	10.8	352	12	US-09-814-353-21234	Sequence 21234, A	c 512	27	10.8	509	11	US-09-918-995-24565	Sequence 24565, A
C 440	27	10.8	357	10	US-09-747-835A-17	Sequence 1282, Ap	c 513	27	10.8	509	12	US-09-814-353-19495	Sequence 19495, A
C 441	27	10.8	364	10	US-09-747-835A-17	Sequence 1282, Ap	c 514	27	10.8	512	12	US-09-814-353-5072	Sequence 5072, Ap
C 442	27	10.8	365	12	US-09-814-353-19505	Sequence 19505, A	c 515	27	10.8	512	12	US-09-814-353-11364	Sequence 11364, A
C 443	27	10.8	373	12	US-10-027-632-256782	Sequence 256782,	c 516	27	10.8	516	12	US-09-814-353-20387	Sequence 20387, A
C 444	27	10.8	373	12	US-10-027-632-256782	Sequence 256782,	c 517	27	10.8	517	12	US-09-814-353-1134	Sequence 1134, Ap
C 445	27	10.8	373	13	US-10-027-632-256782	Sequence 256782,	c 518	27	10.8	521	12	US-09-814-353-7500	Sequence 7500, Ap
C 446	27	10.8	373	13	US-10-027-632-256782	Sequence 256782,	c 519	27	10.8	521	13	US-10-027-632-265935	Sequence 265935,
C 447	27	10.8	382	14	US-10-198-846-11789	Sequence 11789, A	c 520	27	10.8	521	13	US-10-027-632-265935	Sequence 265935,
C 448	27	10.8	390	12	US-10-082-828A-87	Sequence 87, Appli	c 521	27	10.8	522	12	US-09-814-353-21041	Sequence 21041, A
C 449	27	10.8	404	12	US-10-012-952A-32	Sequence 32, Appli	c 522	27	10.8	523	14	US-10-198-846-12582	Sequence 12582, A
C 450	27	10.8	416	11	US-09-918-995-14235	Sequence 14235, A	c 523	27	10.8	530	14	US-10-198-846-12663	Sequence 12663, A
C 451	27	10.8	427	9	US-09-886-241-3	Sequence 3, Appli	c 524	27	10.8	535	10	US-09-232-758-76	Sequence 76, Appli
C 452	27	10.8	427	12	US-09-814-353-20416	Sequence 20416, A	c 525	27	10.8	536	11	US-09-918-995-31814	Sequence 31814, A
C 453	27	10.8	427	14	US-10-198-846-12230	Sequence 12230, A	c 526	27	10.8	539	14	US-10-198-846-10883	Sequence 10883, A
C 454	27	10.8	429	12	US-09-814-353-20728	Sequence 20728, A	c 527	27	10.8	544	10	US-09-757-781-45	Sequence 45, Appli



C 528	27	10.8	546	11	US-09-918-995-32404	Sequence 32404, A	C 601	27	10.8	627	10	US-09-833-381-1295	Sequence 1295, Ap
C 529	27	10.8	550	12	US-09-814-353-19825	Sequence 19825, A	602	27	10.8	631	14	US-10-198-846-8336	Sequence 8336, Ap
C 530	27	10.8	551	11	US-09-918-995-26125	Sequence 26125, A	603	27	10.8	636	12	US-10-027-632-281852	Sequence 281852, A
C 531	27	10.8	555	11	US-09-918-995-13190	Sequence 13190, A	604	27	10.8	636	12	US-10-027-632-281852	Sequence 281852, A
C 532	27	10.8	557	11	US-09-918-995-29207	Sequence 29207, A	605	27	10.8	636	13	US-10-027-632-281852	Sequence 281852, A
C 533	27	10.8	559	12	US-09-814-353-2617	Sequence 2617, Ap	606	27	10.8	636	13	US-10-027-632-281852	Sequence 281852, A
C 534	27	10.8	559	12	US-09-814-353-8951	Sequence 8951, Ap	607	27	10.8	637	12	US-10-027-632-217494	Sequence 217494, A
C 535	27	10.8	559	12	US-10-027-632-202971	Sequence 202971, A	608	27	10.8	637	13	US-10-027-632-217494	Sequence 217494, A
C 536	27	10.8	559	12	US-10-027-632-222512	Sequence 222512, A	609	27	10.8	640	9	US-09-771-209-13	Sequence 13, Appl
C 537	27	10.8	559	12	US-10-027-632-222512	Sequence 222512, A	610	27	10.8	640	12	US-09-814-353-2253	Sequence 2253, Ap
C 538	27	10.8	559	13	US-10-027-632-243752	Sequence 243752, A	611	27	10.8	640	12	US-09-814-353-8593	Sequence 8593, Ap
C 539	27	10.8	559	13	US-10-027-632-222512	Sequence 222512, A	612	27	10.8	650	12	US-10-027-632-225998	Sequence 225998, A
C 540	27	10.8	559	13	US-10-027-632-243752	Sequence 243752, A	613	27	10.8	650	12	US-10-027-632-225998	Sequence 225998, A
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C 542	27	10.8	564	11	US-09-918-995-11211	Sequence 11211, A	615	27	10.8	654	13	US-10-027-632-277474	Sequence 277474, A
C 543	27	10.8	564	11	US-09-918-995-16187	Sequence 16187, A	616	27	10.8	655	14	US-10-198-846-9659	Sequence 9659, Ap
C 544	27	10.8	569	11	US-09-918-995-14941	Sequence 14941, A	617	27	10.8	658	14	US-10-198-846-9362	Sequence 9362, Ap
C 545	27	10.8	570	14	US-10-158-646-8	Sequence 8, Appl	618	27	10.8	662	14	US-10-198-846-8045	Sequence 8045, Ap
C 546	27	10.8	570	14	US-10-158-646-8	Sequence 8, Appl	619	27	10.8	664	14	US-10-198-846-8060	Sequence 8060, Ap
C 547	27	10.8	572	12	US-10-027-632-184982	Sequence 184982, A	620	27	10.8	664	14	US-10-198-846-8060	Sequence 8060, Ap
C 548	27	10.8	572	13	US-10-027-632-184982	Sequence 184982, A	621	27	10.8	665	14	US-10-198-846-1717	Sequence 1717, Ap
C 549	27	10.8	572	14	US-10-007-280A-64	Sequence 64, Appl	622	27	10.8	670	12	US-09-814-353-19800	Sequence 19800, A
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C 551	27	10.8	575	11	US-09-918-995-10295	Sequence 10295, A	624	27	10.8	687	9	US-09-962-436-41	Sequence 41, Appl
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C 553	27	10.8	576	12	US-09-814-353-12143	Sequence 12143, A	626	27	10.8	687	12	US-09-960-706-996	Sequence 996, Ap
C 554	27	10.8	578	14	US-10-198-846-13786	Sequence 13786, A	627	27	10.8	687	12	US-10-027-632-280524	Sequence 280524, A
C 555	27	10.8	578	14	US-10-198-846-13786	Sequence 13786, A	628	27	10.8	687	13	US-10-027-632-280524	Sequence 280524, A
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C 557	27	10.8	580	11	US-09-918-995-13250	Sequence 13250, A	630	27	10.8	689	13	US-10-027-632-231169	Sequence 231169, A
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C 559	27	10.8	582	13	US-10-027-632-270293	Sequence 270293, A	632	27	10.8	699	10	US-09-834-975-318	Sequence 318, Appl
C 560	27	10.8	585	12	US-10-027-632-187960	Sequence 187960, A	633	27	10.8	702	14	US-10-198-846-2127	Sequence 2127, Ap
C 561	27	10.8	585	13	US-10-027-632-187960	Sequence 187960, A	634	27	10.8	708	10	US-09-833-381-1258	Sequence 1258, Ap
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C 568	27	10.8	598	12	US-10-027-632-232149	Sequence 232149, A	641	27	10.8	717	13	US-10-027-632-278293	Sequence 278293, A
C 569	27	10.8	598	12	US-10-027-632-232149	Sequence 232149, A	642	27	10.8	726	14	US-10-198-846-10726	Sequence 10726, A
C 570	27	10.8	598	12	US-10-027-632-232151	Sequence 232151, A	643	27	10.8	727	13	US-10-001-879-84	Sequence 84, Appl
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C 572	27	10.8	598	13	US-10-027-632-210421	Sequence 210421, A	645	27	10.8	728	14	US-10-198-846-10458	Sequence 10458, A
C 573	27	10.8	598	13	US-10-027-632-232149	Sequence 232149, A	646	27	10.8	730	12	US-10-259-165-491	Sequence 491, Appl
C 574	27	10.8	598	13	US-10-027-632-232150	Sequence 232150, A	647	27	10.8	734	10	US-09-995-494-13	Sequence 13, Appl
C 575	27	10.8	600	14	US-10-198-846-9355	Sequence 9355, Ap	648	27	10.8	742	9	US-09-910-943-352	Sequence 352, Appl
C 576	27	10.8	602	10	US-09-796-692-7277	Sequence 7277, Ap	649	27	10.8	742	12	US-10-027-632-253983	Sequence 253983, A
C 577	27	10.8	602	12	US-10-027-632-286994	Sequence 286994, A	650	27	10.8	742	12	US-10-027-632-253984	Sequence 253984, A
C 578	27	10.8	602	12	US-10-027-632-286995	Sequence 286995, A	651	27	10.8	742	13	US-10-027-632-253984	Sequence 253984, A
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C 580	27	10.8	602	13	US-10-027-632-286995	Sequence 286995, A	653	27	10.8	744	10	US-09-954-531-1036	Sequence 1036, Ap
C 581	27	10.8	602	14	US-09-814-353-19787	Sequence 19787, Ap	654	27	10.8	754	12	US-10-259-165-588	Sequence 588, Appl
C 582	27	10.8	604	12	US-10-012-952A-36	Sequence 36, Appl	655	27	10.8	762	14	US-10-082-830-133	Sequence 133, Appl
C 583	27	10.8	607	14	US-10-198-846-8124	Sequence 8124, Ap	656	27	10.8	772	12	US-09-814-353-4407	Sequence 4407, Ap
C 584	27	10.8	607	14	US-10-198-846-8124	Sequence 8124, Ap	657	27	10.8	772	12	US-09-814-353-10711	Sequence 10711, A
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C 586	27	10.8	610	12	US-10-027-632-285467	Sequence 285467, A	659	27	10.8	774	12	US-09-814-353-21900	Sequence 21900, A
C 587	27	10.8	610	13	US-10-027-632-285467	Sequence 285467, A	660	27	10.8	777	11	US-09-909-567B-8	Sequence 8, Appl
C 588	27	10.8	611	12	US-10-027-632-224058	Sequence 224058, A	661	27	10.8	780	10	US-09-867-915-27	Sequence 27, Appl
C 589	27	10.8	611	12	US-10-027-632-245041	Sequence 245041, A	662	27	10.8	781	9	US-09-910-943-383	Sequence 383, Appl
C 590	27	10.8	611	13	US-10-027-632-224058	Sequence 224058, A	663	27	10.8	785	12	US-09-814-353-20358	Sequence 20358, A
C 591	27	10.8	611	13	US-10-027-632-245041	Sequence 245041, A	664	27	10.8	785	14	US-10-198-846-11022	Sequence 11022, A
C 592	27	10.8	612	14	US-10-198-846-8479	Sequence 8479, Ap	665	27	10.8	795	14	US-10-198-846-10719	Sequence 10719, A
C 593	27	10.8	612	14	US-10-198-846-8479	Sequence 8479, Ap	666	27	10.8	797	12	US-10-027-632-265690	Sequence 265690, A
C 594	27	10.8	622	14	US-10-054-841-8	Sequence 8, Appl	667	27	10.8	797	13	US-10-027-632-265690	Sequence 265690, A
C 595	27	10.8	622	14	US-10-054-841-8	Sequence 8, Appl	668	27	10.8	799	14	US-10-198-846-4246	Sequence 4246, Ap
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C 597	27	10.8	623	12	US-10-027-632-250371	Sequence 250371, A	670	27	10.8	801	12	US-10-027-632-258008	Sequence 258008, A
C 598	27	10.8	623	13	US-10-027-632-250370	Sequence 250370, A	671	27	10.8	801	13	US-10-027-632-258007	Sequence 258007, A
C 599	27	10.8	623	13	US-10-027-632-250371	Sequence 250371, A	672	27	10.8	801	13	US-10-027-632-258008	Sequence 258008, A
C 600	27	10.8	625	12	US-09-814-353-19436	Sequence 19436, A	673	27	10.8	805	10	US-09-989-920-41	Sequence 41, Appl

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703	27	10.8	847	14	US-10-198-846-7712	Sequence 7712, Ap	776	10.8	1004	13	US-10-001-876-101	Sequence 101, App
704	27	10.8	850	12	US-09-814-353-20285	Sequence 20285, A	777	10.8	1007	13	US-10-202-193-106	Sequence 106, App
705	27	10.8	854	14	US-10-198-846-3031	Sequence 3031, Ap	778	10.8	1012	12	US-10-017-161-461	Sequence 461, App
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707	27	10.8	855	14	US-10-198-846-13201	Sequence 13201, A	780	10.8	1019	13	US-10-001-887-45	Sequence 45, Appl
708	27	10.8	856	12	US-10-017-161-1447	Sequence 1447, Ap	781	10.8	1020	12	US-10-082-828A-36	Sequence 36, Appl
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719	27	10.8	877	14	US-10-011-585A-97	Sequence 97, Appl	792	10.8	1039	12	US-10-017-161-1159	Sequence 1159, Ap
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727	27	10.8	884	13	US-10-027-632-261817	Sequence 261817, A	800	10.8	1069	12	US-10-017-161-991	Sequence 991, App
728	27	10.8	884	13	US-10-027-632-261818	Sequence 261818, A	801	10.8	1069	12	US-10-017-161-1415	Sequence 1415, Ap
729	27	10.8	884	13	US-10-027-632-261815	Sequence 261815, A	802	10.8	1073	14	US-10-198-846-6810	Sequence 6810, Ap
730	27	10.8	889	14	US-10-198-846-9771	Sequence 9771, Ap	803	10.8	1084	12	US-10-017-161-35	Sequence 35, Appl
731	27	10.8	893	14	US-10-198-846-10461	Sequence 10461, A	804	10.8	1086	14	US-10-198-846-10681	Sequence 10681, A
732	27	10.8	895	14	US-10-198-846-7094	Sequence 7094, Ap	805	10.8	1089	10	US-09-954-456-783	Sequence 783, Ap
733	27	10.8	898	12	US-09-814-353-19884	Sequence 19884, A	806	10.8	1089	10	US-09-880-107-2087	Sequence 2087, Ap
734	27	10.8	904	12	US-10-017-161-1391	Sequence 1391, Ap	807	10.8	1089	12	US-09-873-319-385	Sequence 385, App
735	27	10.8	904	12	US-10-027-632-251510	Sequence 251510, A	808	10.8	1089	12	US-09-960-706-617	Sequence 617, App
736	27	10.8	904	12	US-10-027-632-251511	Sequence 251511, A	809	10.8	1091	12	US-09-814-353-19819	Sequence 19819, A
737	27	10.8	904	12	US-10-027-632-251512	Sequence 251512, A	810	10.8	1096	12	US-10-017-161-2315	Sequence 2315, Ap
738	27	10.8	904	13	US-10-027-632-251510	Sequence 251510, A	811	10.8	1099	12	US-10-027-632-255168	Sequence 255168, A
739	27	10.8	904	13	US-10-027-632-251511	Sequence 251511, A	812	10.8	1099	13	US-10-027-632-255168	Sequence 255168, A
740	27	10.8	904	13	US-10-027-632-251512	Sequence 251512, A	813	10.8	1100	12	US-10-027-632-257048	Sequence 257048, A
741	27	10.8	909	14	US-10-198-846-2884	Sequence 2884, Ap	814	10.8	1100	12	US-10-027-632-257049	Sequence 257049, A
742	27	10.8	910	12	US-10-017-161-1425	Sequence 1425, Ap	815	10.8	1100	13	US-10-027-632-257048	Sequence 257048, A
743	27	10.8	910	14	US-10-198-846-4726	Sequence 4726, Ap	816	10.8	1100	13	US-10-027-632-257049	Sequence 257049, A
744	27	10.8	914	14	US-10-198-846-5574	Sequence 5574, Ap	817	10.8	1102	12	US-10-017-161-1287	Sequence 1287, App
745	27	10.8	914	14	US-10-198-846-9029	Sequence 9029, Ap	818	10.8	1107	12	US-10-241-220-52	Sequence 52, Appl
746	27	10.8	917	14	US-10-198-846-7095	Sequence 7095, Ap	819	10.8	1108	12	US-10-017-161-2263	Sequence 2263, Ap



```
c 966      27 10.8 1302 14 US-10-246-098-69
c 967      27 10.8 1310 14 US-10-198-846-12930
c 968      27 10.8 1311 12 US-09-814-353-19812
c 969      27 10.8 1324 12 US-10-017-161-2297
c 970      27 10.8 1333 12 US-10-017-161-1921
c 971      27 10.8 1333 12 US-10-017-161-2111
c 972      27 10.8 1334 12 US-10-027-632-265790
c 973      27 10.8 1334 12 US-10-027-632-265791
c 974      27 10.8 1334 13 US-10-027-632-265790
c 975      27 10.8 1334 13 US-10-027-632-265791
c 976      27 10.8 1345 12 US-10-017-161-1443
c 977      27 10.8 1348 12 US-10-017-161-2075
c 978      27 10.8 1372 12 US-10-017-161-2277
c 979      27 10.8 1375 14 US-10-176-847-33
c 980      27 10.8 1376 12 US-09-971-392-155
c 981      27 10.8 1376 12 US-09-971-392-155
c 982      27 10.8 1387 12 US-10-017-161-2269
c 983      27 10.8 1390 12 US-10-017-161-945
c 984      27 10.8 1395 12 US-09-814-353-21813
c 985      27 10.8 1396 12 US-10-017-161-2373
c 986      27 10.8 1406 14 US-10-198-846-10016
c 987      27 10.8 1411 12 US-10-017-161-2279
c 988      27 10.9 1414 12 US-10-017-161-531
c 989      27 10.8 1417 12 US-10-017-161-2139
c 990      27 10.8 1427 14 US-10-198-846-13745
c 991      27 10.8 1432 14 US-10-198-846-10035
c 992      27 10.8 1433 14 US-10-198-846-4247
c 993      27 10.8 1435 12 US-10-017-161-1953
c 994      27 10.8 1438 12 US-10-017-161-541
c 995      27 10.8 1440 12 US-10-176-464A-66
c 996      27 10.8 1453 9  US-09-349-015-14
c 997      27 10.8 1453 14 US-10-198-846-13730
c 998      27 10.8 1453 15 US-10-219-664-10
c 999      27 10.8 1455 12 US-10-252-157-389
c1000     27 10.8 1457 12 US-09-8-4-353-21594
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## ALIGNMENTS

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RESULT 1
JS-09-978-167-3
Sequence 3, Application US/09978i67
Publication No. US2003067775A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
FILE REFERENCE: CL001303
CURRENT APPLICATION NUMBER: US/09/978,167
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 78785
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(78785)
OTHER INFORMATION: n = A,T,C or G

Query Match 13.1%; Score 33; DB 11; Length 78785;
Best Local Similarity 100.0%; Pred No. 6 4e-08;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 92 AAAAAATCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
|||||
b 69776 AAAAAATCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 69808
```

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RESULT 2
US-10-155-693-21/c
Sequence 21, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
APPLICANT: WEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 1075
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(445)
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1075)
OTHER INFORMATION: No. US20030175876A1e= "1 to 1075 is 1255 to 2330 of Figure 5 He
OTHER INFORMATION: n in position 763 to 801 indicates positions of divergence betw
US-10-155-693-21
```

```
Query Match 12.4%; Score 31; DB 12; Length 1075;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAAACTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
|||||
Db 807 AAAAACTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 777
```

```
RESULT 3
US-10-155-693-46/c
Sequence 46, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
APPLICANT: WEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46
LENGTH: 1076
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
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/ NAME/KEY: misc_feature
/ LOCATION: (586)..(586)
/ OTHER INFORMATION: N in position 586 indicates a position of divergence between dif
/ OTHER INFORMATION: erent receptor clones.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (764)..(802)
/ OTHER INFORMATION: N in positions 764 to 802 indicates positions of divergence betw
/ OTHER INFORMATION: een different receptor clones.
US-10-155-693-46

Query Match          12.4%; Score 31; DB 12; Length 1076;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAATC...NNNNNNNNNNNNNNNNNNNNNNNN 124
    |||||||...|||||
Db 808 AAAATC...NNNNNNNNNNNNNNNNNNNNNNNN 778
    |||||||...|||||

RESULT 4
JS-10-155-693-15/c
Sequence 15, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
APPLICANT: WEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 2157
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(886)
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(2157)
OTHER INFORMATION: No. US20030175876A1e="1 to 2157 is 814 to 2971 of Figure 5 23brd
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1204)..(1242)
OTHER INFORMATION: N in positions 1204 to 1242 indicates positions of divergence bet
OTHER INFORMATION: ween different receptor clones.
S-10-155-693-15

Query Match          12.4%; Score 31; DB 12; Length 2157;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ty 94 AAAATC...NNNNNNNNNNNNNNNNNNNNNNNN 124
    |||||||...|||||
b 1248 AAAATC...NNNNNNNNNNNNNNNNNNNNNNNN 1218
    |||||||...|||||

ESULT 5
S-10-155-693-43/c
Sequence 43, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
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/ APPLICANT: FOX, GARY M.
/ APPLICANT: JING, SHUQIAN
/ APPLICANT: WEN, DUANZHI
/ TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
/ FILE REFERENCE: A-401C
/ CURRENT APPLICATION NUMBER: US/10/155,693
/ CURRENT FILING DATE: 2002-05-24
/ PRIOR APPLICATION NUMBER: US/08/837,199
/ PRIOR FILING DATE: 1997-04-14
/ PRIOR APPLICATION NUMBER: US 60/015,907
/ PRIOR FILING DATE: 1996-04-22
/ PRIOR APPLICATION NUMBER: US 60/017,221
/ PRIOR FILING DATE: 1996-05-09
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 43
/ LENGTH: 2158
/ TYPE: DNA
/ ORGANISM: HUMAN
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1027)..(1027)
/ OTHER INFORMATION: N in position 1027 indicates a position of divergence between c
/ OTHER INFORMATION: ferent receptor clones.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1205)..(1243)
/ OTHER INFORMATION: N in positions 1205 to 1243 indicates positions of divergence
/ OTHER INFORMATION: tween different receptor clones.
US-10-155-693-43

Query Match          12.4%; Score 31; DB 12; Length 2158;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAATC...NNNNNNNNNNNNNNNNNNNNNNNN 124
    |||||||...|||||
Db 1249 AAAATC...NNNNNNNNNNNNNNNNNNNNNNNN 1219
    |||||||...|||||

RESULT 6
US-10-155-693-1/c
Sequence 1, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
APPLICANT: WEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2568
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (540)..(1934)
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2078)..(2078)
OTHER INFORMATION: N in position 2078 indicates a position of divergence between d
OTHER INFORMATION: ferent receptor clones
```

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/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (2107)..(2107)
/ OTHER INFORMATION: N in position 2107 indicates a position of divergence between dif
/ OTHER INFORMATION: ferent receptor clones
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (2241)..(2241)
/ OTHER INFORMATION: N in position 2241 indicates a position of divergence between dif
/ OTHER INFORMATION: ferent receptor clones
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (2250)..(2250)
/ OTHER INFORMATION: N in position 2250 indicates a position of divergence between dif
/ OTHER INFORMATION: ferent receptor clones
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (2256)..(2294)
/ OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence be
/ OTHER INFORMATION: tween different receptor clones
US-10-155-693-1
Query Match 12.4%; Score 31; DB 12; Length 2568;
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
| | | | | | | | | | | | | | | | | | | | | |
DB 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

RESULT 7
US-10-155-693-5/c
; Sequence 5, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 3209
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (510)
; OTHER INFORMATION: note="1 to 510 is -237 to 272 of Fig 5 Hsgr-21bf"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(510)
; OTHER INFORMATION: note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2078)..(2078)
; OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
; OTHER INFORMATION: ferent receptor clones
; FEATURE:
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/ NAME/KEY: misc feature
/ LOCATION: (2256)..(2294)
/ OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence
/ OTHER INFORMATION: ween different receptor clones
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1091)..(1091)
/ OTHER INFORMATION: N in position 1091 indicates any nucleic acid
US-10-155-693-5
Query Match 12.4%; Score 31; DB 12; Length 3209;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
| | | | | | | | | | | | | | | | | | | | | |
DB 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

RESULT 8
US-10-155-693-37/c
; Sequence 37, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 37
; LENGTH: 3209
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1091)..(1091)
; OTHER INFORMATION: N in position 1091 indicates any nucleic acid.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2078)..(2078)
; OTHER INFORMATION: N in position 2078 indicates a position of divergence between
; OTHER INFORMATION: ferent receptor clones.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2256)..(2294)
; OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence
; OTHER INFORMATION: ween different receptor clones.
US-10-155-693-37
Query Match 12.4%; Score 31; DB 12; Length 3209;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
| | | | | | | | | | | | | | | | | | | | | |
DB 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

RESULT 9
US-10-205-951-36
; Sequence 36, Application US/10205951
; Publication No. US20030119026A1
; GENERAL INFORMATION:
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Query Match 12.0%; Score 30; DB 13; Length 583;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;





---

GenCore version 5.1.6  
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M nucleic - nucleic search, using sw model

Run on: November 6, 2003, 04:11:09 ; Search time 1320 Seconds  
(without alignments)  
4621.533 Million cell updates/sec

Title: US-09-960-481-5278  
Perfect score: 251  
Sequence: 1 ggtggcagttgtgtgacaca.....gtaagaaganatcaaccgag 251

Coring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Ord size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est4:\*

13: gb\_est5:\*

14: gb\_est6:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_man:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gssl:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	116	46.2	218	13	BU764411 sas01a10.
2	116	46.2	389	10	BF068522 st83b03.y
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4	116	46.2	457	10	BG041196 sv31a02.y

5	116	46.2	473	10	BE804090
6	116	46.2	531	12	BM887247
7	116	46.2	554	12	BM891617
8	116	46.2	575	12	BM093555
9	116	46.2	578	12	BM866347
10	116	46.2	580	12	BM520189
11	116	46.2	582	12	BM731308
12	116	46.2	593	13	BU764490
13	101	40.2	565	12	BI893295
14	92	36.7	458	13	BU090543
15	91	36.3	564	12	BM085196
16	91	36.3	619	10	BF324448
17	87	34.7	569	12	BM891461
18	47	18.7	185	13	BU764474
19	47	18.7	577	12	BI893407
20	39	15.5	645	14	CA847674
21	35	13.9	554	10	BE609805
22	35	13.9	558	13	BQ251639
23	35	13.9	572	13	BU082080
24	35	13.9	579	12	BI471007
25	35	13.9	587	12	BM520093
26	35	13.9	632	10	BF425570
27	35	13.9	933	13	BU0905266
28	33	13.1	312	14	CB696715
29	33	13.1	385	29	AL761464
30	33	13.1	401	14	CB769926
31	33	13.1	458	14	CB739092
32	33	13.1	728	29	AG007623
33	33	13.1	779	13	BU534947
34	33	13.1	888	13	BU953716
35	32	12.7	299	14	CB701272
36	32	12.7	314	14	CB709356
37	32	12.7	380	14	CB810722
38	32	12.7	395	14	CB773644
39	32	12.7	398	14	CB707550
40	32	12.7	406	14	CB808056
41	32	12.7	437	14	CB791110
42	32	12.7	441	14	CB748611
43	32	12.7	480	14	CB728742
44	32	12.7	488	14	CB726310
45	32	12.7	496	14	CB713043
46	32	12.7	497	13	BU535280
47	32	12.7	515	14	CB716599
48	32	12.7	516	14	CB546176
49	32	12.7	540	13	BU962138
50	32	12.7	545	14	CB611813
51	32	12.7	556	13	BU953117
52	32	12.7	564	13	BU936799
53	32	12.7	566	14	CB616610
54	32	12.7	575	14	CB608187
55	32	12.7	580	14	CB606923
56	32	12.7	582	14	CB586738
57	32	12.7	670	13	BU403272
58	32	12.7	679	13	BU944423
59	32	12.7	717	13	BQ889272
60	32	12.7	752	12	BM450354
61	32	12.7	754	28	AQ501508
62	32	12.7	757	13	BU841803
63	32	12.7	779	14	CA465859
64	32	12.7	787	14	CA463682
65	32	12.7	836	14	CA463300
66	32	12.7	848	13	BU946418
67	32	12.7	850	13	BU406138
68	32	12.7	872	13	BU172412
69	32	12.7	915	28	AQ744063
70	32	12.7	916	13	BQ430076
71	32	12.7	1034	12	BM904119
72	32	12.7	1063	12	BM452427
73	31	12.4	276	14	CB547776
74	31	12.4	292	14	CB710099
75	31	12.4	311	14	CB696953
76	31	12.4	323	14	CA455545
77	31	12.4	345	10	AW976514

BE804090	sr75fi2.y
BM887247	sam36a12.
BM891617	sam41g03.
BM093555	saj10e11.
BM866347	saj15d12.
BM520189	sak90b05.
BM731308	sai170c07.
BU764490	sas02c05.
BI893295	sai64a12.
BU090543	su06b06.y
BM085196	saj33e03
BF324448	su24h10.y
BM891461	sam27f05.
BU764474	sas02a05.
BI893407	sai165q07.
CA847674	EST0582.t
BE609805	sq42h06.y
BQ251639	sap63h08.
BU082080	ear04e02.
BI471007	sah92c08.
BM520093	sak88h01.
BF425570	su44d05.y
BU0905266	AGENCOURT
CB696715	AMGNNUC:M
AL761464	Arabidops
CB769926	AMGNNUC:S
CB739092	AMGNNUC:N
AG007623	Homo sapi
BU534947	AGENCOURT
BU953716	AGENCOURT
CB701272	AMGNNUC:N
CB709356	AMGNNUC:N
CB810722	AMGNNUC:N
CB773644	AMGNNUC:M
CB707550	AMGNNUC:S
CB808056	AMGNNUC:N
CB791110	AMGNNUC:N
CB748611	AMGNNUC:M
CB728742	AMGNNUC:N
CB726310	AMGNNUC:M
CB713043	AMGNNUC:N
BU535280	AGENCOURT
CB716599	AMGNNUC:N
CB546176	AMGNNUC:N
BU962138	AGENCOURT
CB611813	AMGNNUC:C
BU953117	AGENCOURT
BU936799	AGENCOURT
CB616610	AMGNNUC:C
CB608187	AMGNNUC:N
CB606923	AMGNNUC:U
CB586738	AMGNNUC:U
BU403272	604136777
BU944423	AGENCOURT
BQ889272	AGENCOURT
BM450354	AGENCOURT
AQ501508	V20C8.mtn
BU841803	AGENCOURT
CA465859	AGENCOURT
CA463682	AGENCOURT
CA463300	AGENCOURT
BU946418	AGENCOURT
BU406138	604136794
BU172412	AGENCOURT
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CB547776	AMGNNUC:N
CB710099	AMGNNUC:N
CB696953	AMGNNUC:S
CA455545	AGENCOURT
AW976514	EST388623

C 78	31	12.4	377	12	BI472052	BI472052 sah98g11.	C 151	30	12.0	292	14	CB710100	CB710100 AMGNNUC:N
C 79	31	12.4	382	14	CB808955	CB808955 AMGNNUC:M	C 152	30	12.0	327	12	BM267776	BM267776 MEST372-A
C 80	31	12.4	385	14	CB809376	CB809376 AMGNNUC:T	C 153	30	12.0	347	14	CB705221	CB705221 AMGNNUC:M
C 81	31	12.4	385	12	BM31244	BM31244 MEST332-D	C 154	30	12.0	356	14	CB813713	CB813713 AMGNNUC:S
C 82	31	12.4	388	14	CB805546	CB805546 AMGNNUC:S	C 155	30	12.0	357	14	CB813006	CB813006 AMGNNUC:N
C 83	31	12.4	396	14	CB773375	CB773375 AMGNNUC:S	C 156	30	12.0	364	13	BU403407	BU403407 604138907
C 84	31	12.4	397	14	CB707903	CB707903 AMGNNUC:S	C 157	30	12.0	375	14	CB691732	CB691732 AMGNNUC:S
C 85	31	12.4	401	14	CB869869	CB869869 AMGNNUC:S	C 158	30	12.0	383	14	CB808920	CB808920 AMGNNUC:M
C 86	31	12.4	403	14	CB812368	CB812368 AMGNNUC:N	C 159	30	12.0	385	14	CB702364	CB702364 AMGNNUC:S
C 87	31	12.4	404	14	CB811546	CB811546 AMGNNUC:S	C 160	30	12.0	390	14	CB778390	CB778390 AMGNNUC:H
C 88	31	12.4	405	14	CB808842	CB808842 AMGNNUC:N	C 161	30	12.0	394	14	CB778390	CB778390 AMGNNUC:H
C 89	31	12.4	410	14	CB803532	CB803532 AMGNNUC:N	C 162	30	12.0	399	14	CB782281	CB782281 AMGNNUC:N
C 90	31	12.4	412	14	CB801678	CB801678 AMGNNUC:S	C 163	30	12.0	404	14	CB706801	CB706801 AMGNNUC:N
C 91	31	12.4	415	14	CB800390	CB800390 AMGNNUC:M	C 164	30	12.0	406	14	CB811533	CB811533 AMGNNUC:N
C 92	31	12.4	424	14	CB796841	CB796841 AMGNNUC:N	C 165	30	12.0	407	14	CB808363	CB808363 AMGNNUC:N
C 93	31	12.4	428	14	CB762449	CB762449 AMGNNUC:N	C 166	30	12.0	409	14	CB771512	CB771512 AMGNNUC:N
C 94	31	12.4	429	14	CB762353	CB762353 AMGNNUC:N	C 167	30	12.0	409	14	CB804639	CB804639 AMGNNUC:N
C 95	31	12.4	431	14	CB758106	CB758106 AMGNNUC:M	C 168	30	12.0	412	14	CB804717	CB804717 AMGNNUC:M
C 96	31	12.4	434	14	CB759078	CB759078 AMGNNUC:S	C 169	30	12.0	412	14	CB801693	CB801693 AMGNNUC:S
C 97	31	12.4	434	14	CB759283	CB759283 AMGNNUC:N	C 170	30	12.0	414	14	CB801991	CB801991 AMGNNUC:N
C 98	31	12.4	437	14	CB791124	CB791124 AMGNNUC:N	C 171	30	12.0	414	14	CB801263	CB801263 AMGNNUC:M
C 99	31	12.4	437	14	CB791127	CB791127 AMGNNUC:M	C 172	30	12.0	416	14	CB768139	CB768139 AMGNNUC:N
C 100	31	12.4	437	14	CB791128	CB791128 AMGNNUC:M	C 173	30	12.0	416	14	CB799596	CB799596 AMGNNUC:S
C 101	31	12.4	437	14	CB791129	CB791129 AMGNNUC:N	C 174	30	12.0	417	14	CB799676	CB799676 AMGNNUC:S
C 102	31	12.4	439	14	CB750459	CB750459 AMGNNUC:N	C 175	30	12.0	417	14	CB766902	CB766902 AMGNNUC:N
C 103	31	12.4	440	14	CB749426	CB749426 AMGNNUC:N	C 176	30	12.0	417	14	CB767005	CB767005 AMGNNUC:T
C 104	31	12.4	442	14	CB747876	CB747876 AMGNNUC:M	C 177	30	12.0	417	14	CB767098	CB767098 AMGNNUC:N
C 105	31	12.4	443	14	CB789256	CB789256 AMGNNUC:S	C 178	30	12.0	419	14	CB764594	CB764594 AMGNNUC:S
C 106	31	12.4	444	14	CB745447	CB745447 AMGNNUC:N	C 179	30	12.0	422	14	CB763303	CB763303 AMGNNUC:N
C 107	31	12.4	448	14	CB745919	CB745919 AMGNNUC:M	C 180	30	12.0	422	14	CB763313	CB763313 AMGNNUC:M
C 108	31	12.4	448	14	CB745920	CB745920 AMGNNUC:M	C 181	30	12.0	424	14	CB796327	CB796327 AMGNNUC:N
C 109	31	12.4	448	14	CB746230	CB746230 AMGNNUC:N	C 182	30	12.0	424	14	CB796506	CB796506 AMGNNUC:N
C 110	31	12.4	450	14	CB742041	CB742041 AMGNNUC:N	C 183	30	12.0	425	14	CB695802	CB695802 AMGNNUC:S
C 111	31	12.4	451	14	CB787129	CB787129 AMGNNUC:M	C 184	30	12.0	425	14	CB695996	CB695996 AMGNNUC:N
C 112	31	12.4	452	14	CB786770	CB786770 AMGNNUC:C	C 185	30	12.0	427	14	CB795000	CB795000 AMGNNUC:N
C 113	31	12.4	453	14	CB785548	CB785548 AMGNNUC:M	C 186	30	12.0	427	14	CB795529	CB795529 AMGNNUC:N
C 114	31	12.4	453	14	CB785643	CB785643 AMGNNUC:N	C 187	30	12.0	430	14	CB761340	CB761340 AMGNNUC:N
C 115	31	12.4	456	14	CB740839	CB740839 AMGNNUC:N	C 188	30	12.0	432	14	CB757583	CB757583 AMGNNUC:N
C 116	31	12.4	457	14	CB739974	CB739974 AMGNNUC:M	C 189	30	12.0	432	14	CB793427	CB793427 AMGNNUC:N
C 117	31	12.4	460	14	CB737801	CB737801 AMGNNUC:M	C 190	30	12.0	435	14	CB793159	CB793159 AMGNNUC:N
C 118	31	12.4	461	14	CB737069	CB737069 AMGNNUC:M	C 191	30	12.0	435	14	CB793167	CB793167 AMGNNUC:N
C 119	31	12.4	461	14	CB737070	CB737070 AMGNNUC:M	C 192	30	12.0	437	14	CB790579	CB790579 AMGNNUC:N
C 120	31	12.4	470	14	CB733464	CB733464 AMGNNUC:N	C 193	30	12.0	439	14	CB750006	CB750006 AMGNNUC:S
C 121	31	12.4	471	14	CB732854	CB732854 AMGNNUC:N	C 194	30	12.0	441	14	CB748292	CB748292 AMGNNUC:S
C 122	31	12.4	481	14	CB728226	CB728226 AMGNNUC:N	C 195	30	12.0	441	14	CB748444	CB748444 AMGNNUC:S
C 123	31	12.4	481	14	CB728277	CB728277 AMGNNUC:N	C 196	30	12.0	441	14	CB748871	CB748871 AMGNNUC:N
C 124	31	12.4	481	14	CB726405	CB726405 AMGNNUC:U	C 197	30	12.0	442	14	CB789895	CB789895 AMGNNUC:M
C 125	31	12.4	496	14	CB712927	CB712927 AMGNNUC:U	C 198	30	12.0	443	14	CB789253	CB789253 AMGNNUC:S
C 126	31	12.4	500	12	BM339997	BM339997 MEST316-G	C 199	30	12.0	443	14	CB789450	CB789450 AMGNNUC:N
C 127	31	12.4	508	11	AY112346	AY112346 Zea mays	C 200	30	12.0	444	14	CB745475	CB745475 AMGNNUC:N
C 128	31	12.4	514	14	CB716558	CB716558 AMGNNUC:S	C 201	30	12.0	444	14	CB788113	CB788113 AMGNNUC:M
C 129	31	12.4	529	12	BM804960	BM804960 AGENCOURT:	C 202	30	12.0	444	14	CB744598	CB744598 AMGNNUC:M
C 130	31	12.4	547	14	CB611484	CB611484 AMGNNUC:S	C 203	30	12.0	445	14	CB744999	CB744999 AMGNNUC:N
C 131	31	12.4	564	14	CB608857	CB608857 AMGNNUC:S	C 204	30	12.0	445	14	AY1996583	AY1996583 701667537
C 132	31	12.4	577	13	BU937181	BU937181 AGENCOURT	C 205	30	12.0	446	14	CB747352	CB747352 AMGNNUC:M
C 133	31	12.4	583	14	CB586275	CB586275 AMGNNUC:N	C 206	30	12.0	446	14	CB747461	CB747461 AMGNNUC:S
C 134	31	12.4	621	14	CB578805	CB578805 AMGNNUC:N	C 207	30	12.0	446	14	CB747611	CB747611 AMGNNUC:N
C 135	31	12.4	641	13	BU403426	BU403426 604139491	C 208	30	12.0	448	14	CB743737	CB743737 AMGNNUC:M
C 136	31	12.4	642	11	AY115523	AY115523 Zea mays	C 209	30	12.0	448	14	CB745838	CB745838 AMGNNUC:N
C 137	31	12.4	643	13	BU400669	BU400669 604138111	C 210	30	12.0	448	14	CB746226	CB746226 AMGNNUC:N
C 138	31	12.4	653	13	BU203050	BU203050 604153296	C 211	30	12.0	448	14	CB742647	CB742647 AMGNNUC:M
C 139	31	12.4	664	11	AY110723	AY110723 Zea mays	C 212	30	12.0	449	14	CB743417	CB743417 AMGNNUC:N
C 140	31	12.4	664	13	BU523671	BU523671 AGENCOURT	C 213	30	12.0	449	14	CB782086	CB782086 AMGNNUC:N
C 141	31	12.4	666	28	BI9475	BI9475 T5N17-T7 TA	C 214	30	12.0	450	14	CB742379	CB742379 AMGNNUC:N
C 142	31	12.4	683	14	CB556669	CB556669 AMGNNUC:U	C 215	30	12.0	450	14	CB742433	CB742433 AMGNNUC:N
C 143	31	12.4	745	12	BM474479	BM474479 AGENCOURT	C 216	30	12.0	450	14	CB742508	CB742508 AMGNNUC:N
C 144	31	12.4	837	12	BM552063	BM552063 AGENCOURT	C 217	30	12.0	450	14	CB787734	CB787734 AMGNNUC:N
C 145	31	12.4	877	11	AY111658	AY111658 Zea mays	C 218	30	12.0	451	14	CB786939	CB786939 AMGNNUC:N
C 146	31	12.4	882	13	BU589046	BU589046 AGENCOURT	C 219	30	12.0	451	14	CB787261	CB787261 AMGNNUC:M
C 147	31	12.4	1173	11	AY110202	AY110202 Zea mays	C 220	30	12.0	451	14	CB785671	CB785671 AMGNNUC:N
C 148	31	12.4	1209	11	AY109337	AY109337 Zea mays	C 221	30	12.0	453	14	CB741976	CB741976 AMGNNUC:N
C 149	31	12.4	2474	11	AY110115	AY110115 Zea mays	C 222	30	12.0	454	14	CB785069	CB785069 AMGNNUC:M
C 150	30	12.0	292	14	CB709955	CB709955 AMGNNUC:C	C 223	30	12.0	454	14	CB741754	CB741754 AMGNNUC:N

224	30	12.0	456	14	CB740462	AMGNNUC:N	297	30	12.0	688	13	BU208148	604152062
c 225	30	12.0	456	14	CB741014	AMGNNUC:N	298	30	12.0	691	11	AY11071	Zea mays
c 226	30	12.0	457	14	CB740335	AMGNNUC:M	c 299	30	12.0	701	28	AZ132431	OSJNB006
c 227	30	12.0	458	12	BQ049078	AGENCOURT	300	30	12.0	708	29	AG045940	Pan trogl
c 228	30	12.0	458	14	CB738912	AMGNNUC:N	c 301	30	12.0	726	12	BM550939	AGENCOURT
c 229	30	12.0	458	14	CB739318	AMGNNUC:N	c 302	30	12.0	730	12	BM555987	AGENCOURT
c 230	30	12.0	459	14	CB738723	AMGNNUC:M	c 303	30	12.0	732	12	BI885751	ZF637-1-0
c 231	30	12.0	460	14	CB605719	AMGNNUC:M	c 304	30	12.0	732	12	BM550333	AGENCOURT
c 232	30	12.0	460	14	CB738102	AMGNNUC:M	c 305	30	12.0	733	12	BM915584	AGENCOURT
c 233	30	12.0	461	14	CB737134	AMGNNUC:N	306	30	12.0	757	29	CC313852	TAM32-23B
c 234	30	12.0	462	14	CB736551	AMGNNUC:M	c 307	30	12.0	759	12	BM559074	AGENCOURT
c 235	30	12.0	464	13	BU943807	AGENCOURT	c 308	30	12.0	767	12	BI887945	ZF637-1-0
c 236	30	12.0	464	14	CB734626	AMGNNUC:M	c 309	30	12.0	769	13	BU211897	604156588
c 237	30	12.0	466	14	CB714668	AMGNNUC:N	310	30	12.0	778	13	BU557518	AGENCOURT
c 238	30	12.0	467	14	CB714218	AMGNNUC:M	311	30	12.0	820	14	CB587576	AGENCOURT
c 239	30	12.0	468	14	CB713720	AMGNNUC:M	312	30	12.0	822	13	BU955562	AGENCOURT
c 240	30	12.0	469	14	CB733616	AMGNNUC:M	313	30	12.0	823	14	CB319085	AGENCOURT
c 241	30	12.0	471	9	AI999037	701516802	c 314	30	12.0	826	14	CA466527	AGENCOURT
c 242	30	12.0	471	14	CB732834	AMGNNUC:N	c 315	30	12.0	829	13	BU557569	AGENCOURT
c 243	30	12.0	472	14	CB730312	AMGNNUC:N	c 316	30	12.0	839	11	AY110457	Zea mays
c 244	30	12.0	473	14	CB729784	AMGNNUC:M	c 317	30	12.0	845	14	CA494546	AGENCOURT
c 245	30	12.0	480	14	CB730758	AMGNNUC:M	318	30	12.0	858	13	BU860780	AGENCOURT
c 246	30	12.0	480	14	CB730761	AMGNNUC:N	c 319	30	12.0	896	13	BQ219362	AGENCOURT
c 247	30	12.0	484	14	CB727422	AMGNNUC:S	c 320	30	12.0	901	13	BU960890	AGENCOURT
c 248	30	12.0	485	14	CB727254	AMGNNUC:N	c 321	30	12.0	915	13	BU167748	AGENCOURT
c 249	30	12.0	486	14	CB726716	AMGNNUC:N	c 322	30	12.0	919	13	BQ220131	AGENCOURT
c 250	30	12.0	489	14	CB725903	AMGNNUC:N	c 323	30	12.0	932	13	BU905290	AGENCOURT
c 251	30	12.0	490	14	CB725829	AMGNNUC:T	c 324	30	12.0	936	13	BU953714	AGENCOURT
c 252	30	12.0	495	13	BQ490657	19-E9134-	c 325	30	12.0	942	13	BQ691840	AGENCOURT
c 253	30	12.0	496	13	BU566201	AGENCOURT	c 326	30	12.0	956	14	CA981788	AGENCOURT
c 254	30	12.0	499	14	CB712410	AMGNNUC:C	327	30	12.0	955	13	BQ423361	AGENCOURT
c 255	30	12.0	501	14	CB711928	AMGNNUC:U	c 328	30	12.0	967	11	AY112367	Zea mays
c 256	30	12.0	506	9	AI996752	701668236	c 329	30	12.0	1022	11	AY110438	Zea mays
c 257	30	12.0	516	13	BU79630	AGENCOURT	c 330	30	12.0	1062	11	AY110203	Zea mays
c 258	30	12.0	522	13	BU842541	AGENCOURT	c 331	30	12.0	1069	11	AY112592	Zea mays
c 259	30	12.0	522	14	CB547859	AMGNNUC:N	c 332	30	12.0	1097	12	BM805283	AGENCOURT
c 260	30	12.0	524	14	H15567	Ym27g06.e1	c 333	30	12.0	1131	29	CC304186	CH261-52J
c 261	30	12.0	538	14	CB717432	AMGNNUC:N	c 334	30	12.0	1135	29	CC304191	CH261-52J
c 262	30	12.0	547	14	CB611480	AMGNNUC:S	335	30	12.0	1251	29	CC268218	CH261-88L
c 263	30	12.0	549	14	CB614742	AMGNNUC:S	336	30	12.0	1318	29	CC188209	CH261-380
c 264	30	12.0	558	13	BU170823	AGENCOURT	c 337	30	12.0	1324	14	CB206108	AGENCOURT
c 265	30	12.0	561	13	BU927700	AGENCOURT	c 338	30	12.0	1373	29	CC235146	AGENCOURT
c 266	30	12.0	566	13	BU349082	604171508	c 339	30	12.0	1387	29	CC212250	CH261-170
c 267	30	12.0	567	13	BQ680045	AGENCOURT	c 340	30	12.0	1448	29	CC185035	CH261-170
c 268	30	12.0	572	13	BU199957	604154237	c 341	30	12.0	1450	29	CC210982	CH261-170
c 269	30	12.0	575	14	CB608071	AMGNNUC:C	c 342	30	12.0	1465	29	CC289673	CH261-171
c 270	30	12.0	586	11	AY111527	Zea mays	c 343	30	12.0	1480	29	CC297119	CH261-177
c 271	30	12.0	587	14	CB585351	AMGNNUC:U	c 344	30	12.0	1523	29	CC194564	CH261-170
c 272	30	12.0	590	14	CB583641	AMGNNUC:N	c 345	30	12.0	1545	29	CC288560	CH261-170
c 273	30	12.0	593	14	CB584413	AMGNNUC:N	346	30	12.0	1604	29	CC246351	CH261-360
c 274	30	12.0	602	14	CB582118	AMGNNUC:S	347	30	12.0	1671	14	CA993999	Al126 Pst
c 275	30	12.0	606	14	CB591346	AMGNNUC:N	348	30	12.0	1722	11	AY109704	Zea mays
c 276	30	12.0	613	14	CA741402	wiaic.pk0	349	30	12.0	2590	11	AY109999	Zea mays
c 277	30	12.0	615	13	BQ072464	AGENCOURT	350	30	12.0	3459	11	AY110274	Zea mays
c 278	30	12.0	621	11	AY110363	Zea mays	c 351	29	11.6	155	29	AL947166	Arabidops
c 279	30	12.0	623	13	BU848039	AGENCOURT	352	29	11.6	186	11	AY112556	Zea mays
c 280	30	12.0	624	14	CB578292	AMGNNUC:S	353	29	11.6	236	29	BX288589	Arabidops
c 281	30	12.0	628	13	BQ228319	AGENCOURT	c 354	29	11.6	239	13	BU812742	UL64PH03
c 282	30	12.0	632	13	BU162460	AGENCOURT	c 355	29	11.6	259	29	CC466898	CH240_136
c 283	30	12.0	638	13	BU161381	AGENCOURT	c 356	29	11.6	282	14	CB547768	AMGNNUC:N
c 284	30	12.0	640	13	BU806762	AGENCOURT	c 357	29	11.6	287	14	CB710982	AMGNNUC:N
c 285	30	12.0	641	11	AY111029	Zea mays	358	29	11.6	291	14	CB710264	AMGNNUC:N
c 286	30	12.0	641	13	BU961267	AGENCOURT	359	29	11.6	296	13	BU443795	604142567
c 287	30	12.0	644	14	CB576214	AMGNNUC:S	360	29	11.6	299	14	CB701239	AMGNNUC:N
c 288	30	12.0	650	13	BU292429	604166118	361	29	11.6	300	14	CB701087	AMGNNUC:M
c 289	30	12.0	655	11	AY110518	Zea mays	362	29	11.6	301	14	CB700803	AMGNNUC:N
c 290	30	12.0	658	13	BQ678921	AGENCOURT	363	29	11.6	301	14	CB700829	AMGNNUC:N
c 291	30	12.0	661	11	AY112329	Zea mays	364	29	11.6	301	14	CB700905	AMGNNUC:C
c 292	30	12.0	665	28	AZ527391	267PbA05	365	29	11.6	310	14	CB697072	AMGNNUC:C
c 293	30	12.0	666	14	CB781548	AMGNNUC:N	c 366	29	11.6	310	14	CB697116	AMGNNUC:C
c 294	30	12.0	672	13	BU406808	604138022	367	29	11.6	320	14	CB707973	AMGNNUC:T
c 295	30	12.0	685	14	CB556651	AMGNNUC:Y	368	29	11.6	334	29	BX532968	Arabidops
c 296	30	12.0	686	14	CB556616	AMGNNUC:Y	369	29	11.6	335	14	CB547298	AMGNNUC:S

C 370	29	11.6	344	12	B1887933	B1887933	2F637-1-0	443	29	11.6	408	14	CB771084	CB771084	AMGNNUC:S
C 371	29	11.6	349	14	CB781401	AMGNNUC:U		444	29	11.6	408	14	CB771140	AMGNNUC:S	
C 372	29	11.6	356	13	B0423453	AGENCOURT		C 445	29	11.6	409	14	CB805012	AMGNNUC:N	
C 373	29	11.6	358	14	CB813717	AMGNNUC:S		C 446	29	11.6	409	14	CB805042	AMGNNUC:S	
C 374	29	11.6	358	14	CB812857	AMGNNUC:H		C 447	29	11.6	409	14	CB805042	AMGNNUC:S	
C 375	29	11.6	375	13	B0963392	AGENCOURT		C 448	29	11.6	410	13	BU960114	AGENCOURT	
C 376	29	11.6	375	14	CB691577	AMGNNUC:S		C 449	29	11.6	410	14	CB803687	AMGNNUC:S	
C 377	29	11.6	376	14	CB691130	AMGNNUC:N		C 450	29	11.6	410	14	CB804127	AMGNNUC:N	
C 378	29	11.6	376	14	CB691175	AMGNNUC:M		C 451	29	11.6	411	14	CB803085	AMGNNUC:M	
C 379	29	11.6	376	14	CB782353	AMGNNUC:C		C 452	29	11.6	411	14	CB803086	AMGNNUC:N	
C 380	29	11.6	380	14	CB810241	AMGNNUC:S		C 453	29	11.6	412	14	CB801630	AMGNNUC:N	
C 381	29	11.6	380	14	CB810567	AMGNNUC:S		C 454	29	11.6	415	14	CB800292	AMGNNUC:M	
C 382	29	11.6	382	29	BX286979	Arabidops		C 455	29	11.6	415	14	CB800588	AMGNNUC:S	
C 383	29	11.6	383	14	CB704080	AMGNNUC:S		C 456	29	11.6	415	14	CB800873	AMGNNUC:C	
C 384	29	11.6	383	14	CB704166	AMGNNUC:N		C 457	29	11.6	416	13	BU960872	AGENCOURT	
C 385	29	11.6	384	14	CB703101	AMGNNUC:N		C 458	29	11.6	416	14	CB767508	AMGNNUC:Y	
C 386	29	11.6	384	14	CB703525	AMGNNUC:M		C 459	29	11.6	416	14	CB767738	AMGNNUC:N	
C 387	29	11.6	384	29	AL950592	Arabidops		C 460	29	11.6	416	14	CB768060	AMGNNUC:N	
C 388	29	11.6	387	14	CB806188	AMGNNUC:S		C 461	29	11.6	417	11	AY112507	Zea mays	
C 389	29	11.6	387	14	CB806199	AMGNNUC:N		C 462	29	11.6	417	14	CB766771	AMGNNUC:N	
C 390	29	11.6	388	14	CB805573	AMGNNUC:M		C 463	29	11.6	417	14	CB767136	AMGNNUC:N	
C 391	29	11.6	388	14	CB805583	AMGNNUC:M		C 464	29	11.6	417	14	CB767282	AMGNNUC:S	
C 392	29	11.6	389	14	CB778716	AMGNNUC:S		C 465	29	11.6	417	14	CB767361	AMGNNUC:N	
C 393	29	11.6	389	14	CB778756	AMGNNUC:C		C 466	29	11.6	418	14	CB765482	AMGNNUC:N	
C 394	29	11.6	389	14	CB778776	AMGNNUC:S		C 467	29	11.6	418	14	CB765607	AMGNNUC:S	
C 395	29	11.6	389	14	CB779222	AMGNNUC:S		C 468	29	11.6	418	14	CB765786	AMGNNUC:N	
C 396	29	11.6	389	14	CB779222	AMGNNUC:S		C 469	29	11.6	418	14	CB766123	AMGNNUC:S	
C 397	29	11.6	390	14	CB777782	AMGNNUC:N		C 470	29	11.6	419	14	CB764895	AMGNNUC:N	
C 398	29	11.6	390	14	CB777896	AMGNNUC:N		C 471	29	11.6	419	14	CB799478	AMGNNUC:N	
C 399	29	11.6	390	14	CB778077	AMGNNUC:N		C 472	29	11.6	420	14	CB798307	AMGNNUC:N	
C 400	29	11.6	390	14	CB778499	AMGNNUC:N		C 473	29	11.6	420	14	CB798574	AMGNNUC:N	
C 401	29	11.6	391	14	CB775618	AMGNNUC:S		C 474	29	11.6	420	14	CB798706	AMGNNUC:N	
C 402	29	11.6	392	14	CB774641	AMGNNUC:S		C 475	29	11.6	420	14	CB798748	AMGNNUC:N	
C 403	29	11.6	392	14	CB775033	AMGNNUC:N		C 476	29	11.6	420	14	CB799003	AMGNNUC:N	
C 404	29	11.6	392	14	CB775066	AMGNNUC:M		C 477	29	11.6	421	14	CA494607	AGENCOURT	
C 405	29	11.6	393	14	CB774197	AMGNNUC:S		C 478	29	11.6	421	14	CB764229	AMGNNUC:N	
C 406	29	11.6	393	14	CB774198	AMGNNUC:S		C 479	29	11.6	421	14	CB764416	AMGNNUC:N	
C 407	29	11.6	394	14	CB776785	AMGNNUC:N		C 480	29	11.6	421	14	CB797570	AMGNNUC:N	
C 408	29	11.6	395	12	BM281734	BM281734	k119506.Y	C 481	29	11.6	421	29	AL769168	Arabidops	
C 409	29	11.6	395	14	CB773588	AMGNNUC:U		C 482	29	11.6	421	29	AL769168	Arabidops	
C 410	29	11.6	395	14	CB773780	AMGNNUC:N		C 483	29	11.6	422	13	BU531732	AGENCOURT	
C 411	29	11.6	395	14	CB776143	AMGNNUC:T		C 484	29	11.6	422	14	CB763220	AMGNNUC:N	
C 412	29	11.6	395	14	CB776285	AMGNNUC:S		C 485	29	11.6	422	14	CB763538	AMGNNUC:N	
C 413	29	11.6	396	14	CB772739	AMGNNUC:S		C 486	29	11.6	422	14	CB763931	AMGNNUC:N	
C 414	29	11.6	399	14	CB7706336	AMGNNUC:M		C 487	29	11.6	423	14	CB762757	AMGNNUC:N	
C 415	29	11.6	399	14	CB706274	AMGNNUC:N		C 488	29	11.6	423	14	CB796941	AMGNNUC:S	
C 416	29	11.6	399	14	CB782667	AMGNNUC:H		C 489	29	11.6	423	14	CB796944	AMGNNUC:S	
C 417	29	11.6	400	14	CB544380	AMGNNUC:N		C 490	29	11.6	423	14	CB796951	AMGNNUC:N	
C 418	29	11.6	400	14	CB699736	AMGNNUC:M		C 491	29	11.6	423	14	CB797160	AMGNNUC:M	
C 419	29	11.6	401	14	CB769994	AMGNNUC:S		C 492	29	11.6	424	14	CB795963	AMGNNUC:N	
C 420	29	11.6	401	14	CB770030	AMGNNUC:S		C 493	29	11.6	424	14	CB796057	AMGNNUC:N	
C 421	29	11.6	402	14	CB769674	AMGNNUC:M		C 494	29	11.6	424	14	CB796197	AMGNNUC:N	
C 422	29	11.6	402	14	CB769789	AMGNNUC:M		C 495	29	11.6	425	14	CB696022	AMGNNUC:M	
C 423	29	11.6	402	29	AL763221	Arabidops		C 496	29	11.6	425	14	CB696361	AMGNNUC:N	
C 424	29	11.6	403	14	CB768244	AMGNNUC:N		C 497	29	11.6	425	14	CB696409	AMGNNUC:S	
C 425	29	11.6	403	14	CB768443	AMGNNUC:N		C 498	29	11.6	425	14	CB795842	AMGNNUC:M	
C 426	29	11.6	403	14	CB768644	AMGNNUC:M		C 499	29	11.6	426	14	CB695390	AMGNNUC:N	
C 427	29	11.6	403	14	CB768824	AMGNNUC:M		C 500	29	11.6	427	12	BM078430	MEST119-B	
C 428	29	11.6	405	14	CB808523	AMGNNUC:N		C 501	29	11.6	427	14	CB794692	AMGNNUC:N	
C 429	29	11.6	405	14	CB808544	AMGNNUC:N		C 502	29	11.6	427	14	CB794770	AMGNNUC:N	
C 430	29	11.6	405	14	CB808554	AMGNNUC:S		C 503	29	11.6	427	14	CB794785	AMGNNUC:N	
C 431	29	11.6	405	14	CB808627	AMGNNUC:N		C 504	29	11.6	427	14	CB794892	AMGNNUC:U	
C 432	29	11.6	405	14	CB810881	AMGNNUC:N		C 505	29	11.6	427	14	CB795075	AMGNNUC:N	
C 433	29	11.6	405	14	CB811078	AMGNNUC:S		C 506	29	11.6	428	14	CB794021	AMGNNUC:N	
C 434	29	11.6	405	14	CB811278	AMGNNUC:N		C 507	29	11.6	428	14	CB794464	AMGNNUC:S	
C 435	29	11.6	406	14	CB807477	AMGNNUC:C		C 508	29	11.6	428	14	CB794478	AMGNNUC:N	
C 436	29	11.6	406	14	CB808186	AMGNNUC:N		C 509	29	11.6	428	14	CB794484	AMGNNUC:S	
C 437	29	11.6	406	14	CB808450	AMGNNUC:Y		C 510	29	11.6	428	14	CB794541	AMGNNUC:M	
C 438	29	11.6	407	14	CB771387	AMGNNUC:N		C 511	29	11.6	428	14	CB794585	AMGNNUC:N	
C 439	29	11.6	407	14	CB771662	AMGNNUC:N		C 512	29	11.6	430	14	CB758556	AMGNNUC:M	
C 440	29	11.6	408	14	CB770894	AMGNNUC:M		C 513	29	11.6	430	14	CB758659	AMGNNUC:N	
C 441	29	11.6	408	14	CB770954	AMGNNUC:N		C 514	29	11.6	430	14	CB760807	AMGNNUC:M	
C 442	29	11.6	408	14	CB770976	AMGNNUC:N		C 515	29	11.6	431	14	CB757847	AMGNNUC:M	

C 516	29	11.6	431	14	CB757883	CB757883	AMGNNUC:N	C 589	29	11.6	449	14	CB742958	AMGNNUC:N
C 517	29	11.6	431	14	CB758223	CB758223	AMGNNUC:S	C 590	29	11.6	449	14	CB743037	AMGNNUC:N
C 518	29	11.6	431	14	CB758348	CB758348	AMGNNUC:N	C 591	29	11.6	449	14	CB743143	AMGNNUC:N
C 519	29	11.6	431	14	CB758352	CB758352	AMGNNUC:N	C 592	29	11.6	449	14	CB743245	AMGNNUC:M
C 520	29	11.6	431	14	CB758389	CB758389	AMGNNUC:M	C 593	29	11.6	449	14	CB743389	AMGNNUC:S
C 521	29	11.6	432	14	CB757172	CB757172	AMGNNUC:N	C 594	29	11.6	449	14	CB743396	AMGNNUC:S
C 522	29	11.6	432	14	CB760570	CB760570	AMGNNUC:S	C 595	29	11.6	450	11	AY111591	Zea mays
C 523	29	11.6	432	14	CB760603	CB760603	AMGNNUC:S	C 596	29	11.6	450	14	CB742325	AMGNNUC:M
C 524	29	11.6	433	14	CB759608	CB759608	AMGNNUC:M	C 597	29	11.6	450	14	CB787699	AMGNNUC:N
C 525	29	11.6	433	14	CB759889	CB759889	AMGNNUC:N	C 598	29	11.6	450	14	CB787748	AMGNNUC:M
C 526	29	11.6	433	14	CB760143	CB760143	AMGNNUC:S	C 599	29	11.6	451	14	CB786888	AMGNNUC:N
C 527	29	11.6	433	14	CB760215	CB760215	AMGNNUC:S	C 600	29	11.6	451	14	CB787047	AMGNNUC:N
C 528	29	11.6	434	14	CB758816	CB758816	AMGNNUC:N	C 601	29	11.6	451	14	CB787301	AMGNNUC:M
C 529	29	11.6	434	14	CB759238	CB759238	AMGNNUC:N	C 602	29	11.6	451	14	CB787398	AMGNNUC:N
C 530	29	11.6	434	14	CB759389	CB759389	AMGNNUC:N	C 603	29	11.6	451	14	CB787401	AMGNNUC:M
C 531	29	11.6	434	14	CB793518	CB793518	AMGNNUC:N	C 604	29	11.6	451	14	CB787431	AMGNNUC:M
C 532	29	11.6	434	14	CB793655	CB793655	AMGNNUC:N	C 605	29	11.6	451	14	CB787467	AMGNNUC:N
C 533	29	11.6	434	14	CB793674	CB793674	AMGNNUC:N	C 606	29	11.6	451	14	CB787585	AMGNNUC:N
C 534	29	11.6	434	14	CB793688	CB793688	AMGNNUC:N	C 607	29	11.6	452	14	CB786462	AMGNNUC:N
C 535	29	11.6	435	9	A1994349	701514769		C 608	29	11.6	452	14	CB786555	AMGNNUC:N
C 536	29	11.6	435	14	CB793326	AMGNNUC:N		C 609	29	11.6	453	14	CB547596	AMGNNUC:M
C 537	29	11.6	435	14	CB793327	AMGNNUC:N		C 610	29	11.6	453	14	CB785344	AMGNNUC:N
C 538	29	11.6	436	9	A19943421	701496255		C 611	29	11.6	453	14	CB785494	AMGNNUC:N
C 539	29	11.6	436	14	CB791913	CB791913	AMGNNUC:N	C 612	29	11.6	453	14	CB785850	AMGNNUC:N
C 540	29	11.6	436	14	CB792173	CB792173	AMGNNUC:N	C 613	29	11.6	453	14	CB785859	AMGNNUC:N
C 541	29	11.6	436	14	CB792290	CB792290	AMGNNUC:S	C 614	29	11.6	453	14	CB785890	AMGNNUC:M
C 542	29	11.6	437	14	CB791003	CB791003	AMGNNUC:M	C 615	29	11.6	453	14	CB785913	AMGNNUC:N
C 543	29	11.6	437	14	CB791095	CB791095	AMGNNUC:N	C 616	29	11.6	455	14	CB741311	AMGNNUC:N
C 544	29	11.6	437	14	CB791186	CB791186	AMGNNUC:N	C 617	29	11.6	455	14	CB741435	AMGNNUC:M
C 545	29	11.6	437	14	CB791306	CB791306	AMGNNUC:S	C 618	29	11.6	455	14	CB741556	AMGNNUC:N
C 546	29	11.6	438	14	CB751214	AMGNNUC:N		C 619	29	11.6	455	14	CB741576	AMGNNUC:N
C 547	29	11.6	438	14	CB789974	CB789974	AMGNNUC:N	C 620	29	11.6	455	14	CB741647	AMGNNUC:M
C 548	29	11.6	438	14	CB790241	CB790241	AMGNNUC:N	C 621	29	11.6	455	14	CB741664	AMGNNUC:T
C 549	29	11.6	438	14	CB790393	CB790393	AMGNNUC:N	C 622	29	11.6	455	14	CB741754	AMGNNUC:N
C 550	29	11.6	439	14	CB750731	CB750731	AMGNNUC:N	C 623	29	11.6	455	14	CB741893	AMGNNUC:M
C 551	29	11.6	440	14	CB749322	AMGNNUC:S		C 624	29	11.6	455	14	CB741927	AMGNNUC:N
C 552	29	11.6	440	14	CB749335	AMGNNUC:N		C 625	29	11.6	456	14	CB606191	AMGNNUC:N
C 553	29	11.6	440	14	CB749465	CB749465	AMGNNUC:N	C 626	29	11.6	456	14	CB740617	AMGNNUC:M
C 554	29	11.6	440	14	CB749619	CB749619	AMGNNUC:N	C 627	29	11.6	456	14	CB740753	AMGNNUC:N
C 555	29	11.6	440	14	CB749703	CB749703	AMGNNUC:N	C 628	29	11.6	456	14	CB740891	AMGNNUC:N
C 556	29	11.6	440	14	CB749715	CB749715	AMGNNUC:M	C 629	29	11.6	456	14	CB740978	AMGNNUC:N
C 557	29	11.6	440	14	CB749860	CB749860	AMGNNUC:N	C 630	29	11.6	456	14	CB782065	AMGNNUC:H
C 558	29	11.6	441	14	CB748104	CB748104	AMGNNUC:N	C 631	29	11.6	457	14	CA844479	hac14e08
C 559	29	11.6	441	14	CB748700	CB748700	AMGNNUC:N	C 632	29	11.6	457	14	CB739617	AMGNNUC:M
C 560	29	11.6	442	14	CB747816	CB747816	AMGNNUC:N	C 633	29	11.6	457	14	CB740106	AMGNNUC:N
C 561	29	11.6	442	14	CB789800	CB789800	AMGNNUC:N	C 634	29	11.6	457	14	CB740137	AMGNNUC:N
C 562	29	11.6	442	14	CB789824	CB789824	AMGNNUC:N	C 635	29	11.6	457	14	CB740315	AMGNNUC:N
C 563	29	11.6	443	12	BM335644	NEST164-F		C 636	29	11.6	457	14	CB740332	AMGNNUC:N
C 564	29	11.6	443	14	CB788789	CB788789	AMGNNUC:N	C 637	29	11.6	458	10	AM950730	EST362800
C 565	29	11.6	443	14	CB789001	CB789001	AMGNNUC:N	C 638	29	11.6	458	13	BU927983	AGENCOURT
C 566	29	11.6	443	14	CB789259	CB789259	AMGNNUC:S	C 639	29	11.6	458	14	CB739146	AMGNNUC:N
C 567	29	11.6	443	14	CB789276	CB789276	AMGNNUC:S	C 640	29	11.6	458	14	CB739513	AMGNNUC:N
C 568	29	11.6	443	14	CB789416	CB789416	AMGNNUC:N	C 641	29	11.6	459	14	CB738133	AMGNNUC:N
C 569	29	11.6	444	14	CB547164	CB547164	AMGNNUC:S	C 642	29	11.6	459	14	CB738300	AMGNNUC:M
C 570	29	11.6	444	14	CB745492	CB745492	AMGNNUC:M	C 643	29	11.6	459	14	CB738616	AMGNNUC:N
C 571	29	11.6	444	14	CB788282	CB788282	AMGNNUC:M	C 644	29	11.6	459	14	CB738670	AMGNNUC:N
C 572	29	11.6	444	14	CB788413	CB788413	AMGNNUC:S	C 645	29	11.6	459	14	CB738702	AMGNNUC:N
C 573	29	11.6	445	14	CB546295	CB546295	AMGNNUC:N	C 646	29	11.6	459	14	CB738811	AMGNNUC:N
C 574	29	11.6	445	14	CB744508	CB744508	AMGNNUC:N	C 647	29	11.6	460	13	BO436070	AGENCOURT
C 575	29	11.6	445	14	CB744560	CB744560	AMGNNUC:N	C 648	29	11.6	460	13	BU963308	AGENCOURT
C 576	29	11.6	445	14	CB744753	CB744753	AMGNNUC:N	C 649	29	11.6	460	14	CB737485	AMGNNUC:N
C 577	29	11.6	445	14	CB744840	CB744840	AMGNNUC:N	C 650	29	11.6	460	14	CB737575	AMGNNUC:N
C 578	29	11.6	445	14	CB745085	CB745085	AMGNNUC:M	C 651	29	11.6	460	14	CB738117	AMGNNUC:N
C 579	29	11.6	446	14	CB743913	CB743913	AMGNNUC:N	C 652	29	11.6	461	9	AL720197	AL720197
C 580	29	11.6	446	14	CB744100	CB744100	AMGNNUC:M	C 653	29	11.6	461	13	BU953555	AGENCOURT
C 581	29	11.6	446	14	CB747351	CB747351	AMGNNUC:M	C 654	29	11.6	462	14	CB736611	AMGNNUC:N
C 582	29	11.6	446	14	CB747383	CB747383	AMGNNUC:N	C 655	29	11.6	462	14	CB736646	AMGNNUC:N
C 583	29	11.6	446	14	CB747512	CB747512	AMGNNUC:N	C 656	29	11.6	463	14	CB735281	AMGNNUC:N
C 584	29	11.6	447	14	CB746367	CB746367	AMGNNUC:N	C 657	29	11.6	464	14	CB734646	AMGNNUC:N
C 585	29	11.6	447	14	CB746668	CB746668	AMGNNUC:N	C 658	29	11.6	464	14	CB734749	AMGNNUC:N
C 586	29	11.6	447	14	CB746788	CB746788	AMGNNUC:N	C 659	29	11.6	464	14	CB735267	AMGNNUC:M
C 587	29	11.6	448	14	CB745962	CB745962	AMGNNUC:N	C 660	29	11.6	464	28	AQ151714	HS_3095_A
C 588	29	11.6	449	14	CB742767	CB742767	AMGNNUC:Y	C 661	29	11.6	465	14	CB715134	AMGNNUC:N

C 662	29	11.6	465	14	CB715508	AMGNNUC:N	C 735	29	11.6	528	14	CB719573	AMGNNUC:N
C 663	29	11.6	466	14	CB714611	AMGNNUC:M	C 736	29	11.6	530	13	BU943640	AGENCOURT
C 664	29	11.6	467	14	CB714832	AMGNNUC:N	C 737	29	11.6	531	13	CB718868	AMGNNUC:S
C 665	29	11.6	468	14	CB714901	AMGNNUC:M	C 738	29	11.6	533	13	BU554666	AGENCOURT
C 666	29	11.6	467	14	CB714074	AMGNNUC:N	C 739	29	11.6	534	14	CB545130	AMGNNUC:C
C 667	29	11.6	468	14	CB734128	AMGNNUC:M	C 740	29	11.6	534	14	CB718397	AMGNNUC:N
C 668	29	11.6	468	14	CB734147	AMGNNUC:M	C 741	29	11.6	536	13	BU942831	AGENCOURT
C 669	29	11.6	468	14	CB734338	AMGNNUC:N	C 742	29	11.6	537	13	BU535297	AGENCOURT
C 670	29	11.6	468	14	CB782026	AMGNNUC:Y	C 743	29	11.6	537	13	CB717626	AMGNNUC:N
C 671	29	11.6	469	13	BU534830	AGENCOURT	C 744	29	11.6	540	11	AY112542	Zea mays
C 672	29	11.6	469	14	CB733557	AMGNNUC:N	C 745	29	11.6	540	14	CB612767	AMGNNUC:U
C 673	29	11.6	469	14	CB733595	AMGNNUC:M	C 746	29	11.6	546	28	A2189223	SP 1011 B
C 674	29	11.6	469	14	CB733642	AMGNNUC:N	C 747	29	11.6	550	13	BQ688334	AGENCOURT
C 675	29	11.6	469	14	CB733705	AMGNNUC:N	C 748	29	11.6	552	14	CB614192	AMGNNUC:S
C 676	29	11.6	470	14	CB733013	AMGNNUC:M	C 749	29	11.6	553	14	CB613860	AMGNNUC:U
C 677	29	11.6	470	14	CB733079	AMGNNUC:N	C 750	29	11.6	553	14	CB613963	AMGNNUC:S
C 678	29	11.6	471	14	CB7330645	AMGNNUC:N	C 751	29	11.6	553	14	CB614027	AMGNNUC:N
C 679	29	11.6	471	14	CB7330645	AMGNNUC:N	C 752	29	11.6	554	9	AL963278	AL963278
C 680	29	11.6	472	14	CB546951	AMGNNUC:N	C 753	29	11.6	555	29	AG016512	Homo sapi
C 681	29	11.6	472	14	CB730450	AMGNNUC:N	C 754	29	11.6	558	14	CB610282	AMGNNUC:S
C 682	29	11.6	473	14	CB729860	AMGNNUC:M	C 755	29	11.6	559	12	B1893235	sai163b12
C 683	29	11.6	474	9	AI994429	701496726	C 756	29	11.6	562	13	BQ219227	AGENCOURT
C 684	29	11.6	474	14	CB729285	AMGNNUC:N	C 757	29	11.6	564	14	W26917	16e11 Human
C 685	29	11.6	474	14	CB729377	AMGNNUC:N	C 758	29	11.6	566	14	CB616634	AMGNNUC:U
C 686	29	11.6	474	28	AO865712	r1eb0026G	C 759	29	11.6	567	13	BU851033	AGENCOURT
C 687	29	11.6	475	14	CB729042	AMGNNUC:M	C 760	29	11.6	567	14	CB616361	AMGNNUC:U
C 688	29	11.6	476	13	BQ949365	AGENCOURT	C 761	29	11.6	568	14	CB618179	AMGNNUC:N
C 689	29	11.6	476	14	CB732230	AMGNNUC:M	C 762	29	11.6	571	14	CB615495	AMGNNUC:N
C 690	29	11.6	477	14	CB731243	AMGNNUC:N	C 763	29	11.6	573	14	CB615030	AMGNNUC:S
C 691	29	11.6	478	14	CB731253	AMGNNUC:N	C 764	29	11.6	574	13	BU184818	AGENCOURT
C 692	29	11.6	479	13	BU535379	AMGNNUC:N	C 765	29	11.6	574	14	CB608371	AMGNNUC:U
C 693	29	11.6	479	14	CB730896	AMGNNUC:S	C 766	29	11.6	578	13	BU423232	604145115
C 694	29	11.6	481	14	CB728525	AMGNNUC:N	C 767	29	11.6	582	12	BM074696	MEST296-D
C 695	29	11.6	483	12	BM340423	MEST322-E	C 768	29	11.6	583	12	BM350537	MEST267-E
C 696	29	11.6	487	12	BM267465	MEST367-B	C 769	29	11.6	584	12	BM336112	MEST187-F
C 697	29	11.6	487	13	BU589548	AGENCOURT	C 770	29	11.6	584	14	CB586256	AMGNNUC:N
C 698	29	11.6	487	14	CB726623	AMGNNUC:S	C 771	29	11.6	585	12	AY112046	Zea mays
C 699	29	11.6	488	14	H15553	Ym27e05.s1	C 772	29	11.6	585	11	BM267894	MEST373-F
C 700	29	11.6	488	14	CB726240	AMGNNUC:U	C 773	29	11.6	585	14	CB585867	AMGNNUC:N
C 701	29	11.6	491	9	AI996767	701668292	C 774	29	11.6	589	14	CB583383	AMGNNUC:C
C 702	29	11.6	492	13	BU406049	604137705	C 775	29	11.6	596	14	CB583943	AMGNNUC:N
C 703	29	11.6	492	14	CB546940	AMGNNUC:N	C 776	29	11.6	597	14	CB583045	AMGNNUC:S
C 704	29	11.6	493	14	CB713646	AMGNNUC:N	C 777	29	11.6	598	14	CB582992	AMGNNUC:C
C 705	29	11.6	494	14	CB713438	AMGNNUC:N	C 778	29	11.6	599	11	AY112262	Zea mays
C 706	29	11.6	495	13	BU554578	AGENCOURT	C 779	29	11.6	604	13	BU961396	AGENCOURT
C 707	29	11.6	495	13	BU595930	AGENCOURT	C 780	29	11.6	608	13	BU937469	AGENCOURT
C 708	29	11.6	499	11	AY110677	Zea mays	C 781	29	11.6	610	14	CB580562	AMGNNUC:N
C 709	29	11.6	500	13	BU867420	SP1011 B	C 782	29	11.6	610	14	CB580583	AMGNNUC:N
C 710	29	11.6	501	9	AA495551	c216 Zhou	C 783	29	11.6	612	9	AI996278	701550984
C 711	29	11.6	502	29	AG016501	Homo sapi	C 784	29	11.6	612	14	CB580228	AMGNNUC:N
C 712	29	11.6	503	13	BU345955	604169149	C 785	29	11.6	612	28	A2197900	SP 1035 B
C 713	29	11.6	503	14	CA455726	AGENCOURT	C 786	29	11.6	612	28	BU540219	AGENCOURT
C 714	29	11.6	507	11	AY111917	Zea mays	C 787	29	11.6	613	13	BU540219	AGENCOURT
C 715	29	11.6	507	29	AG016491	Homo sapi	C 788	29	11.6	613	14	CB580141	AMGNNUC:U
C 716	29	11.6	507	29	AL756318	Arabidops	C 789	29	11.6	614	14	CB579876	AMGNNUC:C
C 717	29	11.6	511	9	AW004331	701956478	C 790	29	11.6	616	11	AY110283	Zea mays
C 718	29	11.6	513	12	BM332107	MEST152-E	C 791	29	11.6	618	14	CB579172	AMGNNUC:U
C 719	29	11.6	513	13	BU954499	AGENCOURT	C 792	29	11.6	619	13	BU440391	604147386
C 720	29	11.6	514	13	BU934633	AGENCOURT	C 793	29	11.6	622	14	CB578549	AMGNNUC:N
C 721	29	11.6	515	13	BU174669	AGENCOURT	C 794	29	11.6	622	14	CB578555	AMGNNUC:N
C 722	29	11.6	516	13	BQ689879	AGENCOURT	C 795	29	11.6	623	11	AY111379	Zea mays
C 723	29	11.6	516	14	CB716289	AMGNNUC:U	C 796	29	11.6	624	29	AG016643	Homo sapi
C 724	29	11.6	517	12	BM349215	MEST310-E	C 797	29	11.6	626	13	BU489428	604128147
C 725	29	11.6	517	14	CB716237	AMGNNUC:N	C 798	29	11.6	629	14	CB577605	AMGNNUC:C
C 726	29	11.6	518	13	BU954054	AGENCOURT	C 799	29	11.6	631	29	AG016896	Homo sapi
C 727	29	11.6	518	14	CB715949	AMGNNUC:N	C 800	29	11.6	632	13	BU206678	604153015
C 728	29	11.6	519	13	BU533784	AGENCOURT	C 801	29	11.6	633	11	AY111893	Zea mays
C 729	29	11.6	519	14	CA463709	AGENCOURT	C 802	29	11.6	634	11	AY111941	Zea mays
C 730	29	11.6	521	12	BG810075	mgct002x1	C 803	29	11.6	634	29	AG018510	Homo sapi
C 731	29	11.6	525	13	BU955334	AGENCOURT	C 804	29	11.6	635	29	AG016630	Homo sapi
C 732	29	11.6	526	11	AY111350	Zea mays	C 805	29	11.6	637	12	BM923996	AGENCOURT
C 733	29	11.6	527	13	BU600985	AGENCOURT	C 806	29	11.6	642	13	BU401099	604136701
C 734	29	11.6	527	14	CB719821	AMGNNUC:C	C 807	29	11.6	644	13	BU437841	604144523

C 808	29	11.6	644	29	CC312724	TAM32-22F	C 881	29	11.6	781	13	BU956127	AGENCOURT
C 809	29	11.6	645	13	BU848854	AGENCOURT	882	29	11.6	786	28	AZ186079	SP_1006_A
C 810	29	11.6	645	13	AG018532	Homo sapi	883	29	11.6	786	28	AZ196321	SP_1031_B
C 811	29	11.6	647	11	AY109954	Zea mays	884	29	11.6	790	13	BU929666	AGENCOURT
C 812	29	11.6	647	13	BU601487	AGENCOURT	885	29	11.6	793	14	CD494711	CD412-D01
C 813	29	11.6	649	12	BM336743	WEST198-C	886	29	11.6	794	13	BU860855	AGENCOURT
C 814	29	11.6	649	13	BU558347	AGENCOURT	887	29	11.6	794	14	CA464679	AGENCOURT
C 815	29	11.6	651	14	CB557716	AGNNUC:C	888	29	11.6	797	14	CB781521	AMGNNUC:N
C 816	29	11.6	653	29	AG017573	Homo sapi	889	29	11.6	797	28	AQ749450	HS_5574_A
C 817	29	11.6	655	29	AG018576	Homo sapi	890	29	11.6	799	13	BU937087	AGENCOURT
C 818	29	11.6	656	11	AY111626	Zea mays	891	29	11.6	802	28	BZ036009	oeF84c06
C 819	29	11.6	656	12	BM478204	AGENCOURT	892	29	11.6	804	14	AY110971	Zea mays
C 820	29	11.6	656	13	BQ435823	AGENCOURT	893	29	11.6	804	14	CB229945	AGENCOURT
C 821	29	11.6	657	14	CB557423	AGNNUC:U	894	29	11.6	805	14	CA463139	AGENCOURT
C 822	29	11.6	659	12	BM545980	AGENCOURT	895	29	11.6	809	13	BU567626	AGENCOURT
C 823	29	11.6	661	29	AG018552	Homo sapi	896	29	11.6	812	14	CB314240	AGENCOURT
C 824	29	11.6	663	13	BQ409297	GA_Ed001	897	29	11.6	813	13	BU841960	AGENCOURT
C 825	29	11.6	663	29	AG017631	Homo sapi	898	29	11.6	813	28	AZ133545	OSUNB010
C 826	29	11.6	664	28	BH988217	oeH29a01	899	29	11.6	815	28	AZ187345	SP_1008_B
C 827	29	11.6	669	29	AG014898	Homo sapi	900	29	11.6	824	13	BU599603	AGENCOURT
C 828	29	11.6	671	11	AY110700	Zea mays	901	29	11.6	827	10	BE053823	GA_Ea003
C 829	29	11.6	672	28	BH955736	oeD148g07	902	29	11.6	829	13	BU602111	AGENCOURT
C 830	29	11.6	673	29	CC252330	CH261-15M	903	29	11.6	832	13	BQ691470	AGENCOURT
C 831	29	11.6	673	29	AG017609	Homo sapi	904	29	11.6	836	13	BU601403	AGENCOURT
C 832	29	11.6	676	9	A1910355	IL-BT226-	905	29	11.6	837	28	AQ745358	HS_2276_A
C 833	29	11.6	679	13	BU601923	AGENCOURT	906	29	11.6	839	13	BU602213	AGENCOURT
C 834	29	11.6	680	10	EG440852	GA_Ea001	907	29	11.6	845	13	BQ673897	AGENCOURT
C 835	29	11.6	683	14	CB556679	AMGNNUC:N	908	29	11.6	848	14	CB781513	AGNNUC:N
C 836	29	11.6	685	29	AG018069	Homo sapi	909	29	11.6	849	29	AG120762	Pan trogl
C 837	29	11.6	686	14	CB556629	AMGNNUC:U	910	29	11.6	852	28	BH795465	10D07LL10
C 838	29	11.6	690	29	AG018367	Homo sapi	911	29	11.6	854	29	AG015766	Homo sapi
C 839	29	11.6	692	13	BU506076	AGENCOURT	912	29	11.6	857	29	CNS01809	Drosophil
C 840	29	11.6	696	28	AQ273276	rbxb0029L	913	29	11.6	861	14	CB781503	AGNNUC:N
C 841	29	11.6	696	28	BH927182	oeD148g07	914	29	11.6	863	14	CA464715	AGENCOURT
C 842	29	11.6	698	13	BQ223373	AGENCOURT	915	29	11.6	864	13	BU189870	AGENCOURT
C 843	29	11.6	700	13	BQ228631	AGENCOURT	916	29	11.6	865	11	AY109545	Zea mays
C 844	29	11.6	702	28	AZ200795	SP_1011_A	917	29	11.6	869	11	AY110399	Zea mays
C 845	29	11.6	704	12	BI887516	ZF637-1-0	918	29	11.6	869	12	BM459157	AGENCOURT
C 846	29	11.6	707	29	AG008864	Homo sapi	919	29	11.6	873	13	BU554253	AGENCOURT
C 847	29	11.6	715	12	BM456624	AGENCOURT	920	29	11.6	874	13	BQ439047	AGENCOURT
C 848	29	11.6	715	29	AG016289	Homo sapi	921	29	11.6	878	13	BQ670027	AGENCOURT
C 849	29	11.6	718	13	BQ276397	AGENCOURT	922	29	11.6	878	28	AZ192913	SP_1022_B
C 850	29	11.6	718	13	BU436218	604145275	923	29	11.6	879	12	BI887897	ZF637-1-0
C 851	29	11.6	722	11	AY111372	Zea mays	924	29	11.6	879	13	BU600832	AGENCOURT
C 852	29	11.6	722	28	BH971184	oeD148g07	925	29	11.6	881	10	BE035058	MM02C11_M
C 853	29	11.6	722	28	BH971184	oeD148g07	926	29	11.6	885	13	BU843837	AGENCOURT
C 854	29	11.6	722	29	AG016309	Homo sapi	927	29	11.6	886	14	CB314376	AGENCOURT
C 855	29	11.6	723	13	BU529127	AGENCOURT	928	29	11.6	888	11	AY110623	Zea mays
C 856	29	11.6	724	28	AZ192045	SP_1020_B	929	29	11.6	888	13	BU521349	AGENCOURT
C 857	29	11.6	727	11	AY111186	Zea mays	930	29	11.6	889	13	BQ952397	AGENCOURT
C 858	29	11.6	731	13	BU516803	AGENCOURT	931	29	11.6	890	14	CA988355	AGENCOURT
C 859	29	11.6	733	13	BU942273	AGENCOURT	932	29	11.6	893	13	BU160416	AGENCOURT
C 860	29	11.6	738	13	BU196177	AGENCOURT	933	29	11.6	895	13	BQ430170	AGENCOURT
C 861	29	11.6	741	29	AG018391	Homo sapi	934	29	11.6	899	14	CB781493	AMGNNUC:N
C 862	29	11.6	742	28	BH986636	oeH18g02	935	29	11.6	900	28	AZ174701	SP_0130_A
C 863	29	11.6	742	28	BH986636	oeH18g02	936	29	11.6	901	13	BU963564	AGENCOURT
C 864	29	11.6	743	13	BU563781	AGENCOURT	937	29	11.6	902	13	BU842217	AGENCOURT
C 865	29	11.6	744	14	CA455561	AGENCOURT	938	29	11.6	902	13	BU842217	AGENCOURT
C 866	29	11.6	745	12	BM287558	WEST368-D	939	29	11.6	906	13	BU164521	AGENCOURT
C 867	29	11.6	748	12	BI889086	ZF637-2-0	940	29	11.6	908	28	AQ739004	HS_5384_B
C 868	29	11.6	748	12	BI892168	ZF637-3-0	941	29	11.6	909	11	AY111054	Zea mays
C 869	29	11.6	750	28	BH997260	oeG68d08	942	29	11.6	911	13	BU961153	AGENCOURT
C 870	29	11.6	756	13	BQ927229	AGENCOURT	943	29	11.6	913	14	CA494505	AGENCOURT
C 871	29	11.6	757	13	BU961245	AGENCOURT	944	29	11.6	915	13	BU798845	AGENCOURT
C 872	29	11.6	759	12	BM341661	WEST337-G	945	29	11.6	918	14	CA455626	AGENCOURT
C 873	29	11.6	760	28	BH956646	oeF83a02	946	29	11.6	921	14	CA794081	AGENCOURT
C 874	29	11.6	761	13	BU954442	AGENCOURT	947	29	11.6	925	13	BU409887	AGENCOURT
C 875	29	11.6	767	13	BU857064	AGENCOURT	948	29	11.6	929	13	BU164541	AGENCOURT
C 876	29	11.6	770	13	BU599993	AGENCOURT	949	29	11.6	933	14	CA988761	AGENCOURT
C 877	29	11.6	772	12	BM544455	AGENCOURT	950	29	11.6	949	11	AY112250	Zea mays
C 878	29	11.6	772	29	CC317576	TAM32-3F6	951	29	11.6	953	14	CA986448	AGENCOURT
C 879	29	11.6	779	14	CB208006	AGENCOURT	952	29	11.6	955	14	CA471305	AGENCOURT
C 880	29	11.6	780	11	AY111086	Zea mays	953	29	11.6	957	13	BQ949643	AGENCOURT



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c 954      29 11.6 957 14 CD325113 AGENCOURT
c 955      29 11.6 958 14 CB181369 AGENCOURT
c 956      29 11.6 957 11 AY109993 Zea mays
c 957      29 11.6 967 13 BX431737 AGENCOURT
c 958      29 11.6 968 29 AG080780 Pan trogl
c 959      29 11.6 972 13 BU944399 AGENCOURT
c 960      29 11.6 974 13 BU926652 AGENCOURT
c 961      29 11.6 990 13 BU944424 AGENCOURT
c 962      29 11.6 995 13 BX374301 AGENCOURT
c 963      29 11.6 1000 29 CC253524 CH261-115
c 964      29 11.6 1003 11 AY109801 Zea mays
c 965      29 11.6 1003 13 BU591355 AGENCOURT
c 966      29 11.6 1005 29 CC233173 CH261-87J
c 967      29 11.6 1010 13 BX450807 AGENCOURT
c 968      29 11.6 1013 14 CB562727 AGENCOURT
c 969      29 11.6 1017 13 BU931691 AGENCOURT
c 970      29 11.6 1019 13 BQ891061 AGENCOURT
c 971      29 11.6 1020 11 AY110771 Zea mays
c 972      29 11.6 1023 14 CB231643 AGENCOURT
c 973      29 11.6 1033 13 BX330627 AGENCOURT
c 974      29 11.6 1037 29 CC289660 CH261-13A
c 975      29 11.6 1045 12 BM080518 AGENCOURT
c 976      29 11.6 1048 14 CB320738 AGENCOURT
c 977      29 11.6 1054 10 BE422421 HMM024CF
c 978      29 11.6 1055 13 BU961525 AGENCOURT
c 979      29 11.6 1056 29 CC215744 CH261-189
c 980      29 11.6 1058 11 AY109910 Zea mays
c 981      29 11.6 1061 11 AY110008 Zea mays
c 982      29 11.6 1061 14 CB605930 AMGNNUC:N
c 983      29 11.6 1067 29 CC275375 CH261-76G
c 984      29 11.6 1078 14 CB203689 AGENCOURT
c 985      29 11.6 1079 14 CB202455 AGENCOURT
c 986      29 11.6 1079 29 CC225245 CH261-11D
c 987      29 11.6 1085 12 BM547657 AGENCOURT
c 988      29 11.6 1087 29 CC224160 CH261-114
c 989      29 11.6 1094 12 BM462958 AGENCOURT
c 990      29 11.6 1114 11 AY112169 Zea mays
c 991      29 11.6 1126 12 BM454022 AGENCOURT
c 992      29 11.6 1127 14 CD507381 CDAR4-G02
c 993      29 11.6 1128 12 BQ061453 AGENCOURT
c 994      29 11.6 1129 12 BQ058425 AGENCOURT
c 995      29 11.6 1139 10 BE034978 MN01A01 M
c 996      29 11.6 1155 29 CC214553 CH261-116
c 997      29 11.6 1164 29 CC261365 CH261-72H
c 998      29 11.6 1165 13 BU526465 AGENCOURT
c 999      29 11.6 1168 14 CD500341 CDA44-E03
c1000     29 11.6 1173 10 BE420630 HMM000.H0
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## ALIGNMENTS

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RESULT 1
BU764411 218 bp mRNA linear EST 10-OCT-2002
LOCUS sas01a10.y2 Gm-cl080 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-cl080-2347 5' similar to TR:Q9SW25 Q9SW25 MTN3-LIKE PROTEIN. ;,
mRNA sequence.
BU764411
BU764411.1 GI:23732505
EST. Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 218)
```

```
REFERENCE
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
```

```

R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 128.
FEATURES
Source
1..218
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl080-2347"
/tissue_type="Roots of 8 day old 'Bragg' supernodulating
mutant N-5382 seedlings"
/dev_stage="8 days old"
/lab_host="DH10B"
/notes="Vector: pBluescript II SK-; Site1: EcoRI; Site_2:
XhoI; The mRNA was isolated from roots of 8 day old
'Bragg' supernodulating mutant NTS382 seedlings that were
infected with Bradyrhizobium japonicum, strain USDA 110, 72
hours prior to harvest. Dr. Gary Stacey generously donated
the tissue. The roots were flash-frozen in liquid
nitrogen. Stratagene's cDNA Synthesis kit (catalog number
200401) was used to synthesize the cDNA. First-strand
synthesis was performed with 5'-methyl dCTP, hence the
ligated cDNA was hemimethylated. A modification of
Stratagene's first-strand synthesis primer was used. An
'anchor' nucleotide (V=A, C, or G) was added to the 3' end
of the primer [GAGAGAGAGAGAGAGAGACTAGTTCGAG(T)19V] to
anchor the primer at the 5' end of the poly(A) tract.
After second-strand synthesis, the cDNA ends were filled
in with cloned Pfu DNA, ligated to EcoRI adaptors and
subsequently phosphorylated. The cDNA was then
precipitated and redissolved in sterile, RNase-,
DNase-free water. The XhoI site within the first- strand
synthesis primer was then restricted by digestion with
XhoI from Promega (400/ul); all XhoI sites in the cDNA
would be protected by their hemimethylated status. The
cDNA constructs were size-fractionated with a 500bp
cutoff, using Sephacryl S-500 High Resolution (Pharmacia
Biotech) in a 2-mm diameter column and a bed volume of
approximately 1ml. The column eluent was precipitated,
redissolved, and ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+), vector that
has been digested with EcoRI and XhoI, and phosphorylated
by Stratagene). This library was constructed in the
laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at
Northern Arizona University."
BASE COUNT 60 a 50 c 39 g
ORIGIN
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```

Query Match 46.2%; Score 116; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.9e-50;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 TTCAAAACCATGCCACAGTCATTAAGTTCGCTTTGGATTCTAGGTAACTGTC 184
Db 101 TTCAAAACCATGCCACAGTCATTAAGTTCGCTTTGGATTCTAGGTAACTGTC 160
QY 185 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGA 240
Db 161 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGA 216
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RESULT 2
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OCUS
DEFINITION
  BF068522 389 bp mRNA linear EST 06-DEC-2001
  st83b03.y1 Gm-cl054 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
  Gm-cl054-845 5' similar to TR:P93332 P93332 MTN3 GENE PRECURSOR. ;
  mRNA sequence.
  BF068522 GI:10845385
  BF068522.1 GI:10845385
  EST.
  Glycine max (soybean)
  Glycine max
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
    ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
    Glycine.
  1 (bases 1 to 389)
    Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
    ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
    Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
    ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
    ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
    ,R., Waterston,R. and Wilson,R.
    Public Soybean EST Project
    Unpublished
    Contact: Shoemaker R/Public Soybean EST Project
    Public Soybean EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: est@watson.wustl.edu
    This clone is available through: ResGen, Invitrogen Corp. 2130
    South Memorial Parkway Huntsville, AL 35801 For further information
    call: (800)-533-4363 or contact via email: ccu@resgen.com
    Insert Length: 1390 Std Error: 0.00
    High quality sequence stop: 346.
    Location/Qualifiers
      1..389
        /organism="Glycine max"
        /mol_type="mRNA"
        /db_xref="taxon:3847"
        /clone="GENOME SYSTEMS CLONE ID: Gm-cl054-845"
        /tissue_type="Leaf, 3 week old, greenhouse grown"
        /lab_host="DH10B"
        /clone_lib="Gm-cl054"
        /notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
        XhoI; The Harosoy NIL was constructed and seed was
        provided by Dr. J. Specht, University of Nebraska
        (Shoemaker and Specht, 1995). The cDNA library was
        constructed from mRNA isolated from leaf tissue at various
        developmental stages of 3 week old greenhouse grown
        plants. Complementary DNA was synthesized from mRNA using
        a primer consisting of a poly(dT) sequence with a XhoI
        restriction site and a 3' anchor. EcoRI adapters were
        ligated to the blunt-ended cDNA fragments followed by
        XhoI digestion. The cDNA fragments were directionally
        cloned into the EcoRI-XhoI restriction site of the
        pBluescript vector. The ligated cDNA fragments were
        transformed into DH10B host cells (GibcoBRL). This
        library was constructed in cooperation with Dr. Paul
        Keim's laboratory at Northern Arizona University."
      ASE COUNT 106 a 89 c 73 g 120 t 1 others
      ORIGIN
        Query Match 46.2%; Score 116; DB 10; Length 389;
        Best Local Similarity 100.0%; Pred. No. 3.3e-50;
        Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 125 TTCAAACCATGTCACAGTCATCTAGCTTTGGCTTTGGATTCTAGGTAACTTGC 184
b 110 TTCAAACCATGTCACAGTCATCTAGCTTTGGCTTTGGATTCTAGGTAACTTGC 169

```

```

QY 185 CTCCTTCGCTGCTTTCTGGCCACCACTACCAACATTTTATAGACTTTCTAAGACA 240
Db 170 CTCCTTCGCTGCTTTCTGGCCACCACTACCAACATTTTATAGACTTTCTAAGACA 225

RESULT 3
BU090931
LOCUS
DEFINITION
  BU090931 450 bp mRNA linear EST 29-AUG-2002
  su09e10.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
  Gm-cl066-1004 5' similar to TR:O82587 O82587 MTN3 HOMOLOG. ; mRNA
  sequence.
  BU090931 GI:22541088
  EST.
  Glycine max (soybean)
  Glycine max
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
    ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
    Glycine.
  1 (bases 1 to 450)
    Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
    ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
    Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
    ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
    ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
    ,R., Waterston,R. and Wilson,R.
    Public Soybean EST Project
    Unpublished
    Contact: Shoemaker R/Public Soybean EST Project
    Public Soybean EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: est@watson.wustl.edu
    This clone is available through: Genome Systems, Inc. 4633 World
    Parkway Circle St. Louis, Missouri 63134 For further information
    call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
    427-3324 or contact: clones@genomesystems.com or
    info@genomesystems.com web site: www.genomesystems.com
    High quality sequence stop: 424.
    Location/Qualifiers
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        /mol_type="mRNA"
        /db_xref="taxon:3847"
        /clone="GENOME SYSTEMS CLONE ID: Gm-cl066-1004"
        /tissue_type="Leaf and shoot tip, salt stressed, 2 week
        old seedling"
        /lab_host="DH10B"
        /clone_lib="Gm-cl066"
        /notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
        XhoI; The cDNA library was constructed from mRNA isolated
        from unexpanded leaves and the shoot tips of 2 week old
        seedling from the cultivar Williams. The 2 week old
        seedlings were salt stressed in a solution of 500mM NaCl
        for 3 days prior to harvesting. Complementary DNA was
        synthesized from mRNA using a primer consisting of a
        poly(dT) sequence with a XhoI restriction site. EcoRI
        adapters were ligated to the blunt-ended cDNA fragments
        followed by XhoI digestion. The cDNA fragments were
        directionally cloned into the EcoRI-XhoI restriction site
        of the pBluescript vector. The ligated cDNA fragments were
        transformed into DH10B host cells (GibcoBRL). This library
        was constructed in the laboratory of Dr. Randy
        Shoemaker."
      BASE COUNT 121 a 95 c 90 g 144 t
      ORIGIN
        Query Match 46.2%; Score 116; DB 13; Length 450;
        Best Local Similarity 100.0%; Pred. No. 3.3e-50;

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Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTTGGGATTTCTAGGTAACATTGC 184  
 108 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTTGGGATTTCTAGGTAACATTGC 167

185 CTCCTTCGTGCTCTTCGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGAAGA 240  
 168 CTCCTTCGTGCTCTTCGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGAAGA 223

RESULT 4  
 BG041196  
 LOCUS  
 DEFINITION  
 BG041196.1 GI:12486992  
 EST.  
 Glycine max (soybean)  
 Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE  
 AUTHORS  
 Shoemaker,R., Keim,P., Vodkin,L., Expelling,J., Coryell,V., Khanna  
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
 R., Waterston,R. and Wilson,R.  
 Public Soybean EST Project  
 Unpublished

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information:  
 call: (800)-533-4363 or contact via email: ccu@resgen.com  
 High quality sequence stop: 423.

FEATURES  
 source  
 1. .457  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl057-1155"  
 /tissue\_type="Degenerating cotyledons, 2 week old  
 seedling"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl057"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
 XhoI. The cDNA library was constructed from mRNA isolated  
 from degenerating cotyledons of 2 week old seedlings from  
 PI469916. Complementary DNA was synthesized from mRNA  
 using a primer consisting of a poly(dT) sequence with a  
 XhoI restriction site. EcoRI adapters were ligated to the  
 blunt-ended cDNA fragments followed by XhoI digestion.  
 The cDNA fragments were directionally cloned into the  
 EcoRI-XhoI restriction site of the pBluescript vector. The  
 ligated cDNA fragments were transformed into DH10B host  
 cells (GibcoBRL). This library was constructed in the  
 laboratory of Dr. Randy Shoemaker."

AGE COUNT 126 a 96 c 92 g 143 t  
 RIGIN

Query Match 46.2%; Score 116; DB 10; Length 457;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-50;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTTGGGATTTCTAGGTAACATTGC 184  
 115 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTTGGGATTTCTAGGTAACATTGC 174

185 CTCCTTCGTGCTCTTCGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGAAGA 240  
 175 CTCCTTCGTGCTCTTCGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGAAGA 230

RESULT 5  
 BE804090  
 LOCUS  
 DEFINITION  
 BE804090.1 GI:10235253  
 EST.  
 Glycine max (soybean)  
 Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE  
 AUTHORS  
 Shoemaker,R., Keim,P., Vodkin,L., Expelling,J., Coryell,V., Khanna  
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
 R., Waterston,R. and Wilson,R.  
 Public Soybean EST Project  
 Unpublished

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information:  
 call: (800)-533-4363 or contact via email: ccu@resgen.com  
 Insert Length: 1929 Std Error: 0.00  
 High quality sequence stop: 404.

FEATURES  
 source  
 1. .473  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl052-1608"  
 /tissue\_type="whole seedlings of greenhouse grown plants"  
 /dev\_stage="1 week old"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl052"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
 XhoI. The Harosoy NIL was constructed and seed was  
 provided by Dr. J. Specht, University of Nebraska  
 (Shoemaker and Specht, 1995). The cDNA library was  
 constructed from mRNA isolated from whole seedlings of 1  
 week old greenhouse grown plants. Complementary DNA was  
 synthesized from mRNA using a primer consisting of a  
 poly(dT) sequence with a XhoI restriction site and a 3'  
 anchor. EcoRI adapters were ligated to the blunt-ended  
 cDNA fragments followed by XhoI digestion. The cDNA  
 fragments were directionally cloned into the EcoRI-XhoI  
 restriction site of the pBluescript vector. The ligated  
 cDNA fragments were transformed into DH10B host cells  
 (GibcoBRL). The library was constructed in cooperation  
 with Dr. Paul Keim's laboratory at Northern Arizona  
 University."

```
BASE COUNT      127 a      103 c      99 g      144 t
ORIGIN
Query Match      46.2%; Score 116; DB 10; Length 473;
Best Local Similarity 100.0%; Pred. No. 3.4e-50;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 125 TTCCAAACCATGTCACAGTCATCTAAGTTTCGGCTTTGGGATTTCTAGGTAAACATTGC 184
    |||
b 116 TTCCAAACCATGTCACAGTCATCTAAGTTTCGGCTTTGGGATTTCTAGGTAAACATTGC 175
    |||

y 185 CTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTTGTGAAGAAGA 240
    |||
b 176 CTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTTGTGAAGAAGA 231

RESULT 6
BM887247      531 bp      mRNA      linear      EST 08-MAR-2002
sam36a12.y1 Gm-cl068 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl068-6576 5' similar to TR:082587 082587 MTN3 HOMOLOG. ;, mRNA
sequence.
BM887247      BM887247.1 GI:1927099:
EST.
SOURCE      Glycine max (soybean)
ORGANISM      Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 531)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -4ORP from Gibco
High quality sequence stop: 432.
Location/Qualifiers
1. .531
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl068-6576"
/tissue_type="Leaf, drought stressed, 1 month old plants,
greenhouse grown"
/lab_host="DH10B"
/clone_lib="Gm-cl068"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from drought stressed leaf tissue of the cultivar Williams
82. The month old greenhouse grown plants were deprived of
water for 3 days prior to harvesting the stressed leaf
tissue. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the

FEATURES
source
1. .531
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl068-6576"
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greenhouse grown"
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/clone_lib="Gm-cl068"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from drought stressed leaf tissue of the cultivar Williams
82. The month old greenhouse grown plants were deprived of
water for 3 days prior to harvesting the stressed leaf
tissue. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the

BASE COUNT      141 a      116 c      108 g      166 t
ORIGIN
Query Match      46.2%; Score 116; DB 12; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.5e-50;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 TTCCAAACCATGTCACAGTCATCTAAGTTTCGGCTTTGGGATTTCTAGGTAAACATTGC 184
    |||
Db 101 TTCCAAACCATGTCACAGTCATCTAAGTTTCGGCTTTGGGATTTCTAGGTAAACATTGC 160
    |||

QY 185 CTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTTGTGAAGAAGA 240
    |||
Db 161 CTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTTGTGAAGAAGA 216

RESULT 7
BM891617      554 bp      mRNA      linear      EST 11-MAR-2002
sam41903.y1 Gm-cl068 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl068-7589 5' similar to TR:082587 082587 MTN3 HOMOLOG. ;, mRNA
sequence.
BM891617      BM891617.1 GI:19346737
EST.
SOURCE      Glycine max (soybean)
ORGANISM      Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 554)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -4ORP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
1. .554
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl068-7589"
/tissue_type="Leaf, drought stressed, 1 month old plants,
greenhouse grown"
/lab_host="DH10B"
/clone_lib="Gm-cl068"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from drought stressed leaf tissue of the cultivar Williams
82. The month old greenhouse grown plants were deprived of
water for 3 days prior to harvesting the stressed leaf
tissue. Complementary DNA was synthesized from mRNA using
```

a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 148 a 119 c 113 g 174 t  
 ORIGIN  
 Query Match 46.2%; Score 116; DB 12; Length 554;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-50;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTCGGATTCAGTAAACATTGC 184  
 DB 113 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTCGGATTCAGTAAACATTGC 172

QY 185 CTCCTTCGTGCTTCTCGGCACCACTACCAACATTTATAGAGTTTGTAGAAGA 240  
 DB 173 CTCCTTCGTGCTTCTCGGCACCACTACCAACATTTATAGAGTTTGTAGAAGA 228

RESULT 8  
 LOCUS 3M093555  
 DEFINITION BM093555 575 bp mRNA linear EST 30-NOV-2001  
 ID: Gm-cl066-2517 5' similar to TR:082587 MTN3 HOMOLOG. ; mRNA sequence.  
 ACCESSION BM093555.1 GI:17022521  
 VERSION  
 KEYWORDS  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 1 (bases 1 to 575)  
 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com  
 High quality sequence stop: 421.  
 Location/Qualifiers  
 1. .575  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl066-2517"  
 /tissue\_type="leaf and shoot tip, salt stressed, 2 week old seedling"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl066"  
 /notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. the 2 week old

FEATURES  
 source

seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 154 a 124 c 116 g 181 t  
 ORIGIN  
 Query Match 46.2%; Score 116; DB 12; Length 575;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-50;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTCGGATTCAGTAAACATTGC 184  
 DB 113 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTCGGATTCAGTAAACATTGC 172

QY 185 CTCCTTCGTGCTTCTCGGCACCACTACCAACATTTATAGAGTTTGTAGAAGA 240  
 DB 173 CTCCTTCGTGCTTCTCGGCACCACTACCAACATTTATAGAGTTTGTAGAAGA 228

RESULT 9  
 LOCUS BM886347  
 DEFINITION BM886347 578 bp mRNA linear EST 08-MAR-2002  
 ID: sam15d12.Y1 Gm-cl068 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-cl068-4799 5' similar to TR:082587 MTN3 HOMOLOG. ; mRNA sequence.  
 ACCESSION BM886347.1 GI:19270091  
 VERSION  
 KEYWORDS  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 1 (bases 1 to 578)  
 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 430.  
 Location/Qualifiers  
 1. .578  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl068-4799"  
 /tissue\_type="leaf, drought stressed, 1 month old plants, greenhouse grown"  
 /lab\_host="DH10B"

FEATURES  
 source

```
/clone lib="Gm-cl068"
/Note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from drought stressed leaf tissue of the cultivar Williams
82. The month old greenhouse grown plants were deprived of
water for 3 days prior to harvesting the stressed leaf
tissue. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
BASE COUNT      151 a 122 c 121 g 183 t      1 others
ORIGIN
Query Match      46.2%; Score 116; DB 12; Length 578;
Best Local Similarity 100.0%; Pred. No. 3.5e-50;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
125 TTCCAAAACCATGCCACAGTCATCTAAGTTTCGGCTTTGGGATTTCTAGGTAACATTGC 184
|||||
97 TTCCAAAACCATGCCACAGTCATCTAAGTTTCGGCTTTGGGATTTCTAGGTAACATTGC 156
|||||
185 CTCCTTCGTGCTTTCTGCGACCACTACCAACATTTTATAGAGTTTGTAAAGAGA 240
|||||
157 CTCCTTCGTGCTTTCTGCGACCACTACCAACATTTTATAGAGTTTGTAAAGAGA 212
|||||

RESULT 10
MS20189
OCUS      580 bp mRNA linear EST 15-FEB-2002
saks90b05.yl Gm-cl057 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl057-2770 5' similar to TR:082587 082587 MTN3 HOMOLOG. ; mRNA
sequence.
MS20189
MS20189.1 GI:18691341
EST.
Glycine max (soybean)
Glycine max
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 580)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Hunttsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
1. .580
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
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/clones="SOYBEAN CLONE ID: Gm-cl057-2770"
/tissue_type="Degenerating cotyledons, 2 week old
seedling"
/lab host="DH10B"
/clone lib="Gm-cl057"
/Note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 2 week old seedlings from
PI468916. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion.
The cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
BASE COUNT      156 a 124 c 119 g 181 t
ORIGIN
Query Match      46.2%; Score 116; DB 12; Length 580;
Best Local Similarity 100.0%; Pred. No. 3.5e-50;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
125 TTCCAAAACCATGCCACAGTCATCTAAGTTTCGGCTTTGGGATTTCTAGGTAACATTGC 184
|||||
115 TTCCAAAACCATGCCACAGTCATCTAAGTTTCGGCTTTGGGATTTCTAGGTAACATTGC 174
|||||
185 CTCCTTCGTGCTTTCTGCGACCACTACCAACATTTTATAGAGTTTGTAAAGAGA 240
|||||
175 CTCCTTCGTGCTTTCTGCGACCACTACCAACATTTTATAGAGTTTGTAAAGAGA 230
|||||

RESULT 11
BM731308
LOCUS      582 bp mRNA linear EST 01-MAR-2002
sal70c07.yl Gm-cl061 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl061-4357 5' similar to TR:082587 082587 MTN3 HOMOLOG. ; mRNA
sequence.
BM731308
BM731308.1 GI:19052641
EST.
Glycine max (soybean)
Glycine max
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 582)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Hunttsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
1. .582
/organism="Glycine max"
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```

/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl061-4357"
/tissue_type="mature flowers of field grown plants"
/lab_host="DH10B"
/clone_lib="Gm-cl061"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

```

```

BASE COUNT 154 a 124 g 122 g 182 t
ORIGIN

```

```

Query Match 46.2%; Score 116; DB 12; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.5e-50;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

125 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCTTTGGGATTTAGGTACATTGC 184
|||||
90 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCTTTGGGATTTAGGTACATTGC 149
|||||
185 CTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTATAGATTTGTAAAGA 240
|||||
150 CTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTATAGATTTGTAAAGA 205
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```

```

RESULT 12
BU764490 593 bp mRNA linear EST 10-OCT-2002
sa02c05.y2 Gm-cl080 Glycine max cDNA clone SOYBEAN CLONE ID: mRNA
Gm-cl080-2434 5' similar to FR:082587 082587 MTN3 HOMOLOG. ;, mRNA
sequence.
BU764490
BU764490.1 GI:23732640

```

```

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

```

```

1 (bases 1 to 593)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
, A., Bolla, B., Marita, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished

```

```

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

```

```

Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com

```

```

Seq primer: -40RP from Gibco
High quality sequence stop: 409.
Location/Qualifiers
1. .593

```

```

FEATURES
source

```

```

/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl080-2434"
/tissue_type="Roots of 8 day old 'Bragg' supernodulating
mutant NTS382 seedlings"
/dev_stages="8 days old"
/lab_host="DH10B"
/clone_lib="Gm-cl080"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The mRNA was isolated from roots of 8 day old
'Bragg' supernodulating mutant NTS382 seedlings that were
infected with Bradyrhizobium japonicum, strain USDA 110.72
hours prior to harvest. Dr. Gary Stacey generously donated
the tissue. The roots were flash-frozen in liquid
nitrogen. Stratagene's cDNA Synthesis Kit (catalog number
200401) was used to synthesize the cDNA. First-strand
synthesis was performed with 5-methyl dCTP, hence the
ligated cDNA was hemimethylated. A modification of
Stratagene's first-strand synthesis primer was used. An
'anchor' nucleotide (V=A, C, or G) was added to the 3' end
of the primer [GAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to
anchor the primer at the 5' end of the poly(A) tract.
After second-strand synthesis, the cDNA ends were filled
in with cloned Pfu DNA, ligated to EcoRI adapters and
subsequently phosphorylated. The cDNA was then
precipitated and redissolved in sterile, RNase-,
DNase-free water. The XhoI site within the first- strand
synthesis primer was then restricted by digestion with
XhoI from Promega (400/ul); all XhoI sites in the cDNA
would be protected by their hemimethylated status. The
cDNA constructs were size-fractionated with a 500bp
cutoff, using Sephacryl S-500 High Resolution (Pharmacia
Biotech) in a 2-mm diameter column and a bed volume of
approximately 1ml. The column eluent was precipitated,
redissolved, and ligated into Stratagene's pBluescript II
XR predigested vector (pBluescript II SK(+)) vector that
has been digested with EcoRI and XhoI, and phosphorylated
by Stratagene). This library was constructed in the
laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at
Northern Arizona University."
BASE COUNT 155 a 128 c 123 g 187 t
ORIGIN

```

```

Query Match 46.2%; Score 116; DB 13; Length 593;
Best Local Similarity 100.0%; Pred. No. 3.5e-50;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

125 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCTTTGGGATTTAGGTACATTGC 184
|||||
92 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCTTTGGGATTTAGGTACATTGC 151
|||||
185 CTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTTGTAAAGA 240
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152 CTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTTGTAAAGA 207
|||||

```

```

RESULT 13
BI893295 565 bp mRNA linear EST 30-NOV-2001
sa164a12.y1 Gm-cl068 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl068-3120 5' similar to FR:082587 082587 MTN3 HOMOLOG. ;,
mRNA sequence.
BI893295
BI893295.1 GI:16105555

```

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Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

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1 (bases 1 to 565)

```





**KEYWORDS**  
 EST.  
 Glycine max (soybean)  
**SOURCE**  
 Glycine max  
**ORGANISM**  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
**REFERENCE**  
 1 (bases 1 to 564)  
 Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
 ,A., Bolla,B., Marras,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
 ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
 ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
 ,R., Waterston,R. and Wilson,R.  
 Public Soybean EST Project  
**TITLE**  
 Public Soybean EST Project  
**JOURNAL**  
 Unpublished  
**COMMENT**  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel.: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact: ccu@resgen.com web site:  
 www.resgen.com  
 High quality sequence stop: 359.

**FEATURES**  
 source  
 Location/Qualifiers  
 1..564  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl066-4446"  
 /tissue\_type="Leaf and shoot tip, salt stressed, 2 week  
 old seedling"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl066"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
 XhoI; The cDNA library was constructed from mRNA isolated  
 from unexpanded leaves and the shoot tips of 2 week old  
 seedling from the cultivar Williams. The 2 week old  
 seedlings were salt stressed in a solution of 500mM NaCl  
 for 3 days prior to harvesting. Complementary DNA was  
 synthesized from mRNA using a primer consisting of a  
 poly(dT) sequence with a XhoI restriction site. EcoRI  
 adapters were ligated to the blunt-ended cDNA fragments  
 followed by XhoI digestion. The cDNA fragments were  
 directionally cloned into the EcoRI-XhoI restriction site  
 of the pBluescript vector. The ligated cDNA fragments were  
 transformed into DH10B host cells (GibcoBRL). This library  
 was constructed in the laboratory of Dr. Randy  
 Shoemaker."

**BASE COUNT** 137 a 124 c 115 g 187 t 1 others  
**ORIGIN**  
 Query Match 36.3%; Score 91; DB 12; Length 564;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-37;  
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 150 CTAAGTTTCGCTTTGGGATTCAGGTACATTCGCTCTCTGCTGCTTTCTGACCA 209  
 Db 1 CTAAGTTTCGCTTTGGGATTCAGGTACATTCGCTCTCTGCTGCTTTCTGACCA 60  
 QY 210 CTACCAACATTTTATAGAGTTTGTAAAGAGA 240  
 Db 61 CTACCAACATTTTATAGAGTTTGTAAAGAGA 91

Search completed: November 6, 2003, 05:05:15  
 Job time : 1368 secs